

sau96I
 avall
 asuI
 fnu4HI accI nlaIV
 286 GTA GCG GCG GAA GTC TAC GGG ACC GAA AGA CAG CCA CGA ACT CAC TAT
 78 Val Ala Ala Glu Val Tyr Gly Thr Glu Arg Gln Pro Arg Thr His Tyr

fnu4HI
 mboII bbvI aluI
 hphI fnu4HI aluI pvuII
 334 TAT GCC GTG GCT GTG GTG AAG AAG GGC GGC AGC TTT CAG CTG AAC GAA
 94 Tyr Ala Val Ala Val Val Lys Lys Gly Gly Ser Phe Gln Leu Asn Glu

haeIII sau96I
 stuI avall
 bglI haeI asuI fokI
 382 CTG CAA GGT CTG AAG TCC TGC CAC ACA GGC CTT CGC AGG ACC GCT GGA
 110 Leu Gln Gly Leu Lys Ser Cys His Thr Gly Leu Arg Arg Thr Ala Gly

sau96I
 avall
 asuI
 nlaIV
 430 TGG AAT GTC CCT ACA GGG ACA CTT CGT CCA TTC TTG AAT TGG ACG GGT
 126 Trp Asn Val Pro Thr Gly Thr Leu Arg Pro Phe Leu Asn Trp Thr Gly

hgiIII aluI
 bsp1286 fnu4HI
 banII bbvI
 ddeI mnlI pvuII mboII aluI pvuII
 478 CCA CCT GAG CCC ATT GAG GCA GCT GTG CAG TTC TTC TCA GCC AGC TGT
 142 Pro Pro Glu Pro Ile Glu Ala Ala Val Gln Phe Phe Ser Ala Ser Cys

mspI
 hpaII
 scrFI
 nciI
 cauII
 526 GTT CCC GGT GCA GAT AAA GGA CAG TTC CCC AAC CTG TGT CGC CTG TGT
 158 Val Pro Gln Ala Asp Lys Gly Gln Phe Pro Asn Leu Cys Arg Leu Cys

nlaIV
 scrFI
 ecoRII
 mnlI bstNI rsaI
 574 GCG GGG ACA GGG GAA AAC AAA TGT GCC TTC TCC TCC CAG GAA CCG TAC
 174 Ala Gly Thr Gly Glu Asn Lys Cys Ala Phe Ser Ser Gln Glu Pro Tyr

FIG.-1

```

                                nlaIV
                                hgiCI
                                aluI      banI      ddeI      bsmal      bsmal
622 TTC AGC TAC TCT GGT GCC TTC AAG TGT CTG AGA GAC GGG GCT GGA GAC
190 Phe Ser Tyr Ser Gly Ala Phe Lys Cys Leu Arg Asp Gly Ala Gly Asp

                                sau96I
                                avall
                                asuI
                                ppuMI
                                hgiAI      ecoD109I
                                bsp1286      mnlI      mnlI
670 GTG GCT TTT ATC AGA GAG AGC ACA GTG TTT GAG GAC CTG TCA GAC GAG
206 Val Ala Phe Ile Arg Glu Ser Thr Val Phe Glu Asp Leu Ser Asp Glu

718 GCT GAA AGG GAC GAG TAT GAG TTA CTC TGC CCA GAC AAC ACT CGG AAG
222 Ala Glu Arg Asp Glu Tyr Glu Leu Leu Cys Pro Asp Asn Thr Arg Lys

                                scrFI
                                nciI
                                mspI
                                hpaII
                                caulI
                                xmaI sau96I
                                smaI nlaIV
                                scrFI
                                nciI avall
                                caulI
                                auaI asuI
                                sau96I ppuMI
                                haeIII nlaIV
                                asuI      ecoD109I      nlaIII
bsrI
766 CCA GTG GAC AAG TTC AAA GAC TGC CAT CTG GCC CGG GTC CCT TCT CAT
238 Pro Val Asp Lys Phe Lys Asp Cys His Leu Ala Arg Val Pro Ser His

                                sfaNI
                                fokI      mboII
                                bglI      draIII      mnlI      hinfI
814 GCC GTT GTG GCA CGA AGT GTG AAT GGC AAG GAG GAT GCC ATC TGG AAT
254 Ala Val Val Ala Arg Ser Val Asn Gly Lys Glu Asp Ala Ile Trp Asn

                                scrFI
                                ecoRII
                                bstNI      hphI
862 CTT CTC CGC CAG GCA CAG GAA AAG TTT GGA AAG GAC AAG TCA CCG AAA
270 Leu Leu Arg Gln Ala Gln Glu Lys Phe Gly Lys Asp Lys Ser Pro Lys

```

FIG.-1

sau3AI
 mboI
 dpnI
 xhoII
 bstYI
 bglII
 aluI
 bstXI
 nlaIV
 910 TTC CAG CTC TTT GGC TCC CCT AGT GGG CAG AAA GAT CTG CTG TTC AAG
 286 Phe Gln Leu Phe Gly Ser Pro Ser Gly Gln Lys Asp Leu Leu Phe Lys

nlaIV
 hgiCI
 pleI
 hinfI
 mnlI bsp1286 mnlI
 taqI banI auaI hinfI
 958 GAC TCT GCC ATT GGG TTT TCG AGG GTG CCC CCG AGG ATA GAT TCT GGG
 302 Asp Ser Ala Ile Gly Phe Ser Arg Val Pro Pro Arg Ile Asp Ser Gly

mspI
 hpaII
 rsaI
 nlaIV
 fokI
 mnlI
 1006 CTG TAC CTT GGC TCC GGC TAC TTC ACT GCC ATC CAG AAC TTG AGG AAA
 318 Leu Tyr Leu Gly Ser Gly Tyr Phe Thr Ala Ile Gln Asn Leu Arg Lys

mspI
 hpaII
 scrFI
 nciI
 fnu4HI
 mnlI
 fnu4HI
 mnlI
 bbvI cauII
 hhaI
 1054 AGT GAG GAG GAA GTG GCT GCC CGG CGT GCG CGG GTC GTG TGG TGT GCG
 344 Ser Glu Glu Glu Val Ala Ala Arg Arg Ala Arg Val Val Trp Cys Ala

hinPI
 mstI
 fspI
 fnu4HI
 aluI hhaI
 bstXI
 alwNI bbvI
 bsrI
 1102 GTG GGC GAG CAG GAG CTG CGC AAG TGT AAC CAG TGG AGT GGC TTG AGC
 350 Val Gly Glu Gln Glu Leu Arg Lys Cys Asn Gln Trp Ser Gly Leu Ser

fnu4HI
 bbvI
 bspMI
 mnlI haeIII
 mnlI
 sfaNI
 1150 GAA GGC AGC GTG ACC TGC TCC TCG GCC TCC ACC ACA GAG GAC TGC ATC
 366 Glu Gly Ser Val Thr Cys Ser Ser Ala Ser Thr Thr Glu Asp Cys Ile

scrFI
 ecoRII
 bstNI
 bstXI
 aluI sfaNI nlaIII
 fokI mnlI
 1198 GCC CTG GTG CTG AAA GGA GAA GCT GAT GCC ATG AGT TTG GAT GGA GGA
 382 Ala Leu Val Leu Lys Gly Glu Ala Asp Ala Met Ser Leu Asp Gly Gly

FIG.-1

nlaiV
hgiCI
banI scrFI

mspI ecoRII
hpaII bstNI

fnu4HI
bbvI

hinPI
hhaI

fnu4HI
bbvI

5096I
n laIV

fnu4HI

50u3A1

```

                                haeIII
                                haeI
                                eaeI          styl
                                ddeI          cfrI      pleI ncol
                                draIII       balI      hinfI
1966 ACC AAA AAC CTT CTG TTC AAT GAC AAC ACT GAG TGT CTG GCC AGA CTC
638 Thr Lys Asn Leu Leu Phe Asn Asp Asn Thr Glu Cys Leu Ala Arg Leu

                                sau96I
                                avall
                                asuI
                                nlaIII      ndeI      sspI      nlaIV
2014 CAT GGC AAA ACA ACA TAT GAA AAA TAT TTG GGA CCA CAG TAT GTC GCA
654 His Gly Lys Thr Thr Tyr Glu Lys Tyr Leu Gly Pro Gln Tyr Val Ala

                                scrFI
                                ecoRII
                                bstNI
                                hgiAI
                                bsp1286      mnlI      mnlI
2062 GGC ATT ACT AAT CGT AAA AAG TGC TCA ACC TCC CCC CTC CTG GAA GCC
670 Gly Ile Thr Asn Leu Lys Lys Cys Ser Thr Ser Pro Leu Leu Glu Ala

                                ddeI
                                mstII
                                mnlI
                                eco8II
                                ecoRI      bsu36I
                                mbolI      sau96I      haeIII
                                mbolI      asuI      aluI
2110 TGT GAA TTC CTC AGG AAG TAA AACCGAAGAA GATGGCCCAG CTCCCCAAGA
685 Cys Glu Phe Leu Arg Lys DC*

                                styl
                                haeIII
                                sau96I
                                asuI
                                mbolI      scrFI
                                earI      ecoRII
                                aluI      bstNI
                                ddeI      mnlI
                                nlaIV
                                ecoD109I nlaIV
2161 AAGCCTCAGC CATTCACTGC CCCAGCTCT TCTCCCAGG TGTGTTGGGG CCTTGGCTCC

                                ddeI
                                ecoNI
                                fokI
2221 CCTGCTGAAG GTGGGGATTG CCCATCCATC TGCTTACAAT TCCCTGCTGT CGTCTTAGCA

2281 AGAAGTAAAA TGAGAAATTT TGTTGATATT CAAAAAAAAA

>LENGTH: 2319

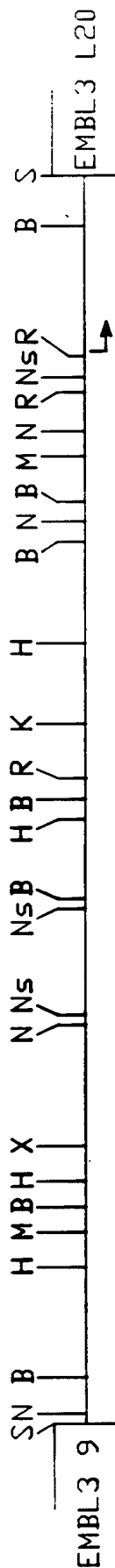
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FIG.-1

215

FIG.-2

1435 TGG AGT GGC TTG AGC GAA GGC AGC GTG ACC GTG TCC TCG GCC TCC ACC ACA GAG GAC TGC ATC GCC CTG GTG CTG AAA GGA GAA GCT
 362 W S G L S E G S V T C S S A S T T E D C I A L V L K G E A
 1522 GAT GCC ATG AGT TTG GAT GGA GGA TAT GTG TAC ACT GCA TGC AAA TGT GGT TTG GTG CCT GTC CTG GCA GAG AAC TAC AAA TCC CAA
 391 D A M S L D G G Y Y T A C K C G L V P V L A E N Y K S Q
 1609 CAA AGC AGT GAC CCT AAC TGT GTG GAT AGA CCT GTG GAA GGA TAT CTT GCT GTG GCG GTG GTT AGG AGA TCA GAC ACT AGC
 420 Q S S D P D P N C V D R P V E G Y L A V A V R S D T S
 1696 CTT ACC TGG AAC TCT GTG AAA GGC AAG AAC TCC TGC CAC ACC GCC GTG GAC AGG ACT GCA GGC TGG AAT ATC CCC ATG GGC CTG CTC
 449 L T W N S V K G K S C N T A V D R T A G V N I P M Q L L
 1783 TTC AAC CAG ACG GGC TCC TGC AAA TTT GAT GAA TAT TTC AGT CAA AGC TGT GCC CCT GGG TCT GAC CCG AGA TCT AAT CTC TGT GCT
 478 F N Q T G S C K F D E Y F S C A P G S D P R S N L C A
 1870 CTG TGT ATT GGC GAC GAG GGT GAG AAT AAG TGC CCC AAC AGC AAC GAG AGA TAC TAC GGC TAC ACT GGG GCT TTC CGG TGC
 507 L C I G D E Q G E N K C V P N S N E R Y Y G Y T G A F R C
 1957 CTG GCT GAG AAT GCT GGA GAC GTT GCA TTT GTG AAA GAT GTG ACT GTC TTG CAG AAC ACT GAT GGA AAT AAC AAT GAG GCA TGG GCT
 536 L A E N A G D V A F V K D V L Q N T D G N N E A W A
 2044 AAG GAT TTG AAC CTG GCA GAC TTT GCG CTG CTG TGC CTC GAT GGC AAA CGG AAG CCT GTG ACT GAC GCT AGA AGC TGC CAT CTT GCC
 565 K D L K L A D F A L L C L D G K R K P V T E A R S C H L A
 2131 ATG GCC CCG AAT CAT GCC GTG TCT CGG ATG GAT AAG GTG GAA CGC CTG AAA CAG GTG CTC CAC CAA CAG GCT AAA TTT GGG
 594 M A P N H A V V S R M D K V E R L K Q V L L H Q Q A K F G
 2218 AGA AAT GGA TCT GAC TGC CCG GAC AAG TTT TGC TTA TTC CAG TCT GAA ACC AAA AAC CTT CTG TTC AAT GAC AAC ACT GAG TGT CTG
 623 R N G S D C P D K F C L F Q S E T K N L L F N D N T E C L
 2305 GCC AGA CTC CAT GGC AAA ACA TAT GAA AAA TAT TTG GGA CCA CAG TAT GTC GCA GGC ATT ACT AAT CTG AAA AAG TGC TCA ACC
 652 A R L H G K T T Y E K Y L G P Q Y V A G I T N L K K C S T
 2392 TCC CCC CTC CTG GAA GCC TGT GAA TTC CTC AGG AAG TAA AACGAAGAA GATGGCCAG CTCGCCAAGA AAGCTCAGC CATTCACTGC CCCCAGCTCT
 681 S P L L E A C E F L R K D
 2491 TCTCCCCAGG TGTGTTGGG CCTTGGCTCC CCTGCTGAAG GTGGGGATTG CCCATCCATC TGCTTACAAT TCCCTGCTGT CGTCTTAGCA AGAAGTAAAA
 2591 TGAGAAATTT TGTGATATT CAAAAAAA

RESTRICTION MAP OF 5' - FLANKING REGION OF α S1 CASEIN GENE

S - SalI

1Kb

B - BstII

R - EcoRI

H - HindIII

M - SmaI

N - NcoI

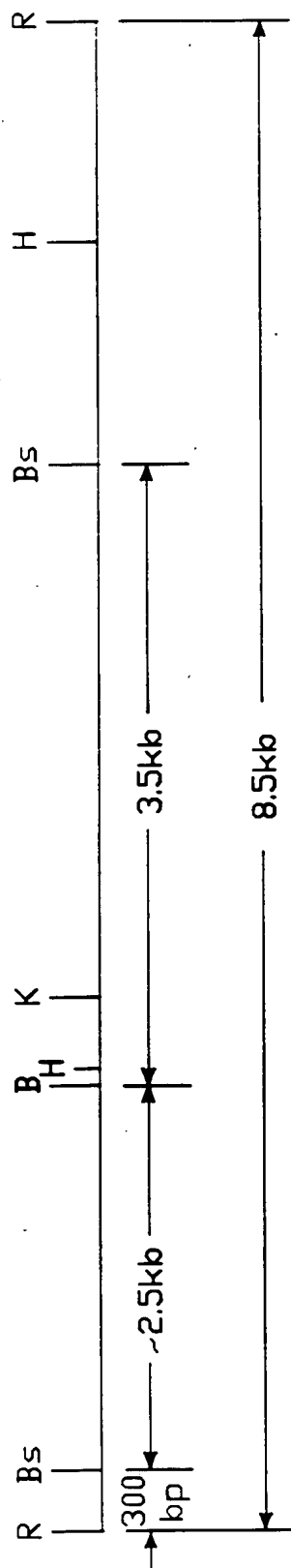
Ns - NsiI

X - XhoI

K - KpnI

FIG.-3

RESTRICTION MAP OF 3' FLANKING
REGION OF α S1 CASEIN GENE



1kb

R - EcoRI
Bs - Bst EII
B - BamHI
H - HindIII
K - KpnI

FIG.-4

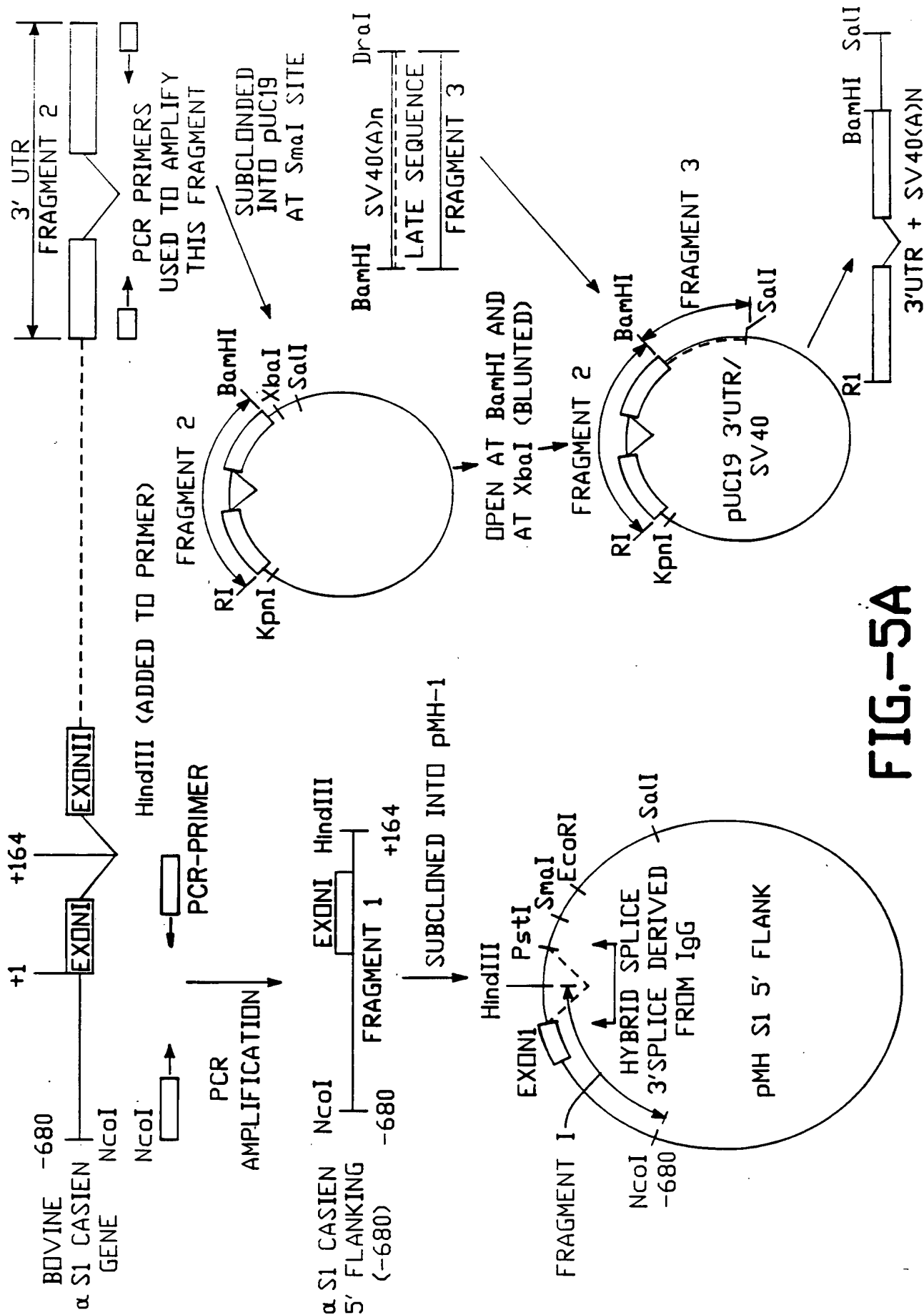


FIG.-5A

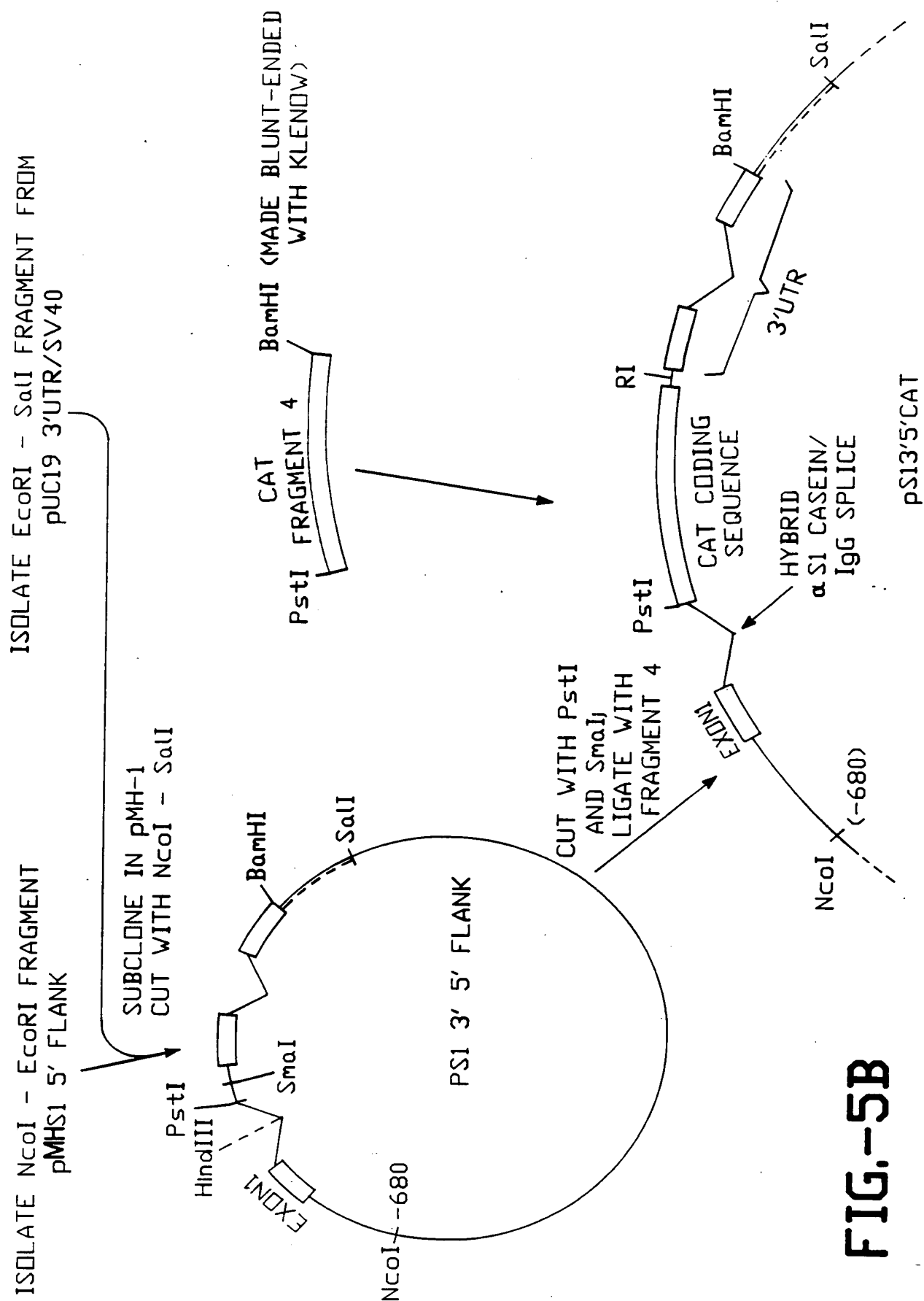
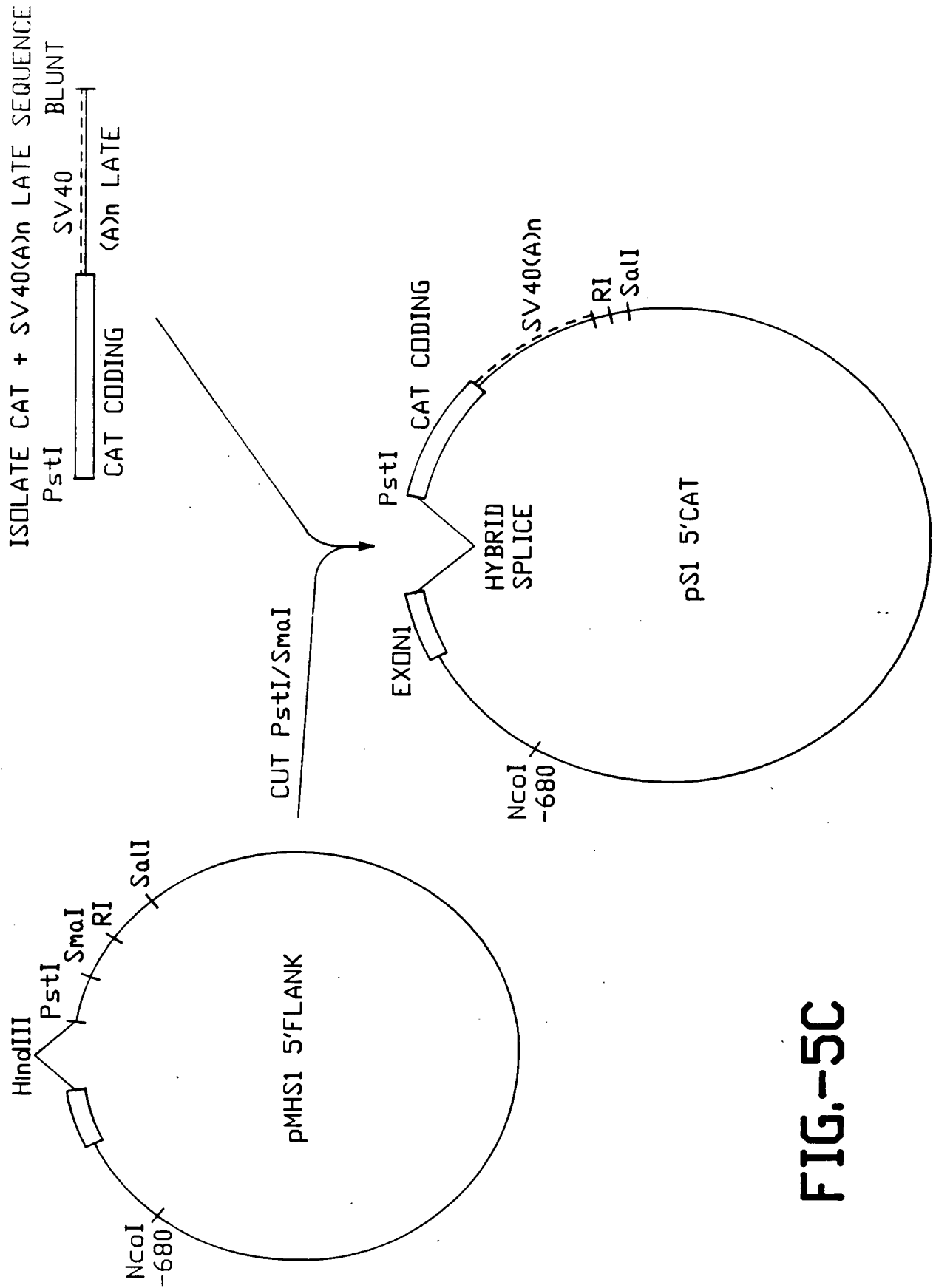


FIG.-5B



NAME pMH-1

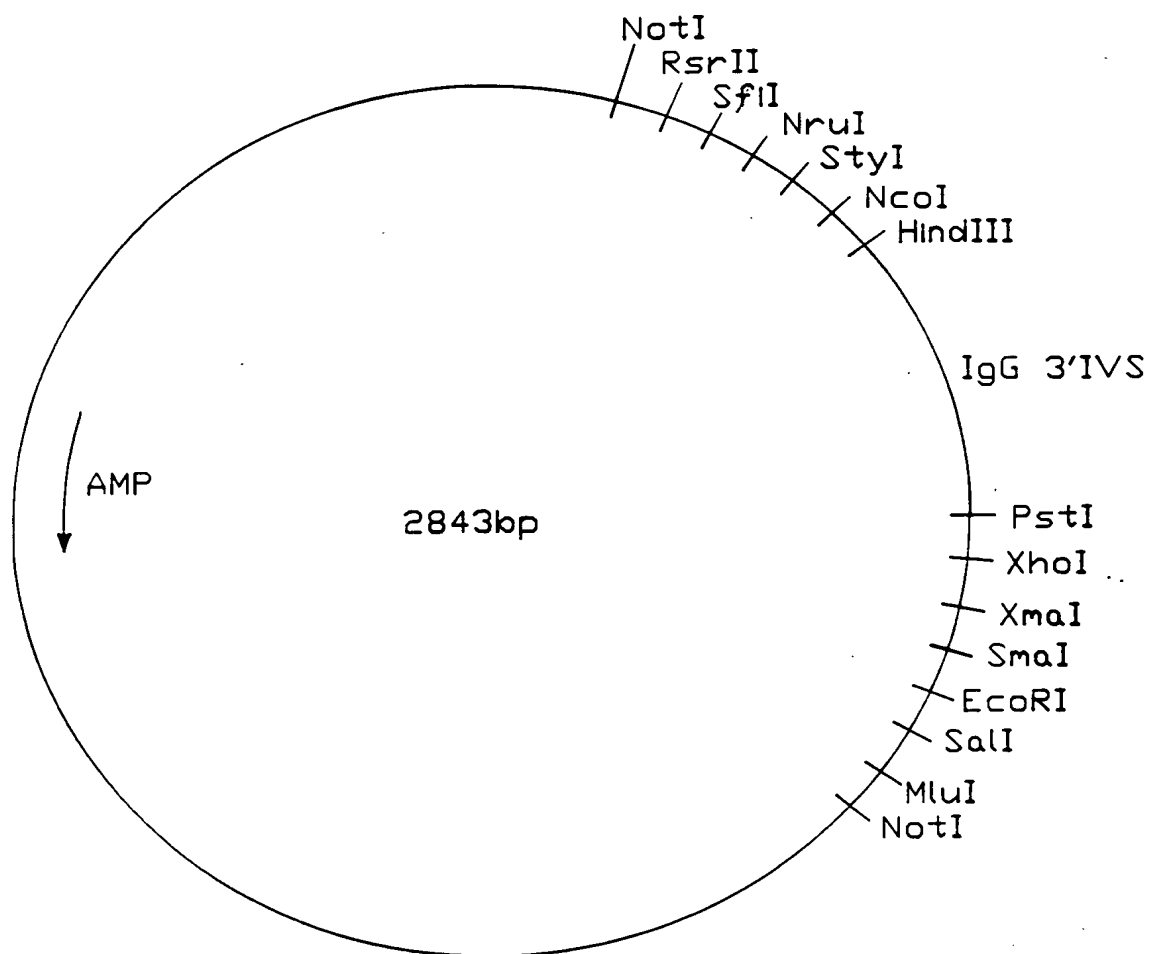
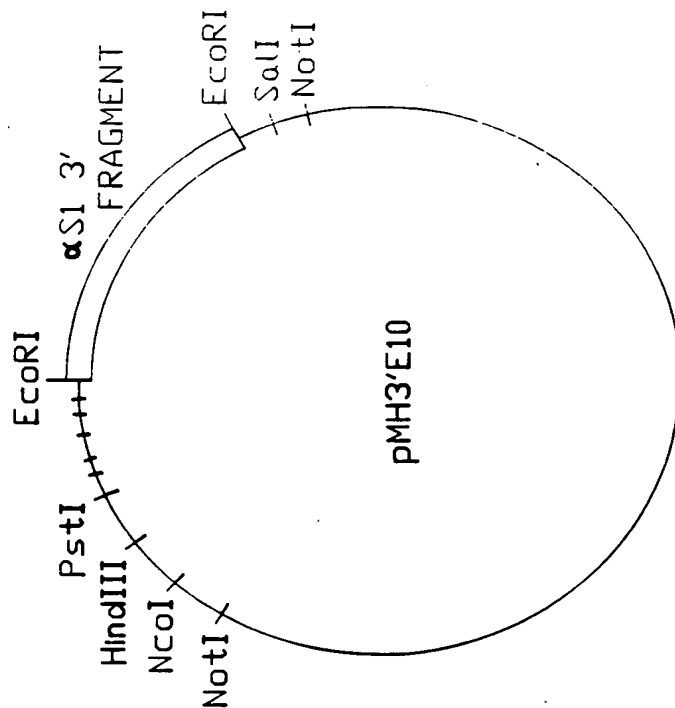
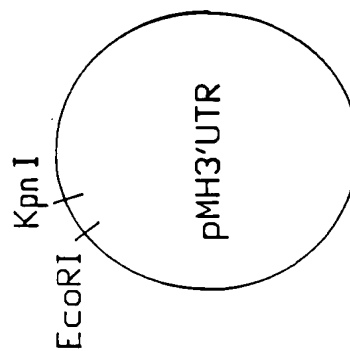


FIG.-6

- PLASMID **PMH3'E10** CONTAINS ~ 8.5Kb **EcoRI** FRAGMENT OF THE 3'-END OF α S1 CASEIN. PMH-1 WAS CUT W/**EcoRI** + LIGATED TO THIS FRAGMENT



- PLASMID **PMH3'UTRhLF2 LINKER**



(FRAGMENT 7)
3' TERMINAL
+ hLF CODING
SEQUENCE
(~ 20bp)

CUT W/**EcoRI**
AND **KpnI**

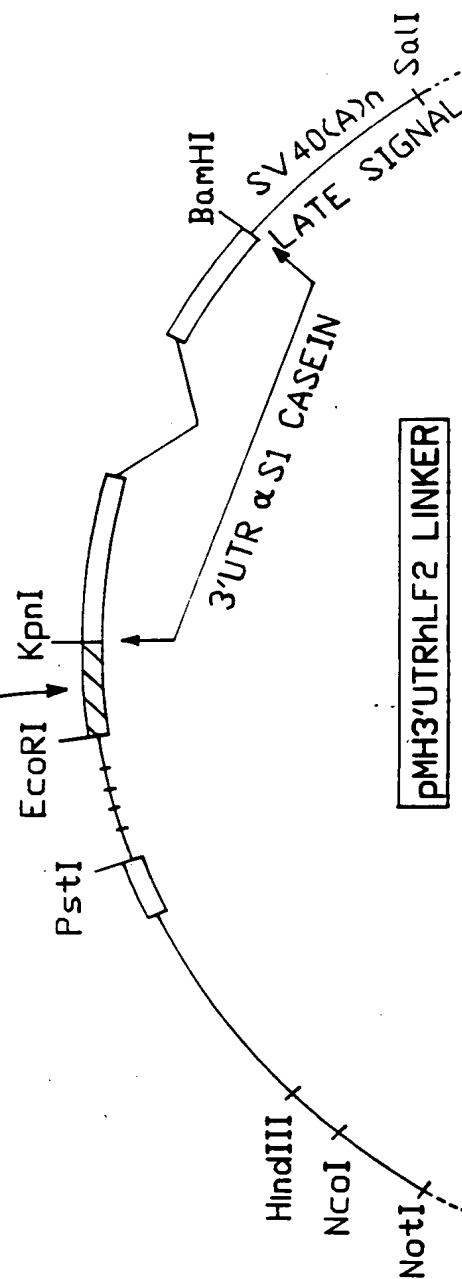


FIG.-7A

PMH3'UTRhLF2 LINKER



CONSTRUCTION OF pS1 3'UTRhLF

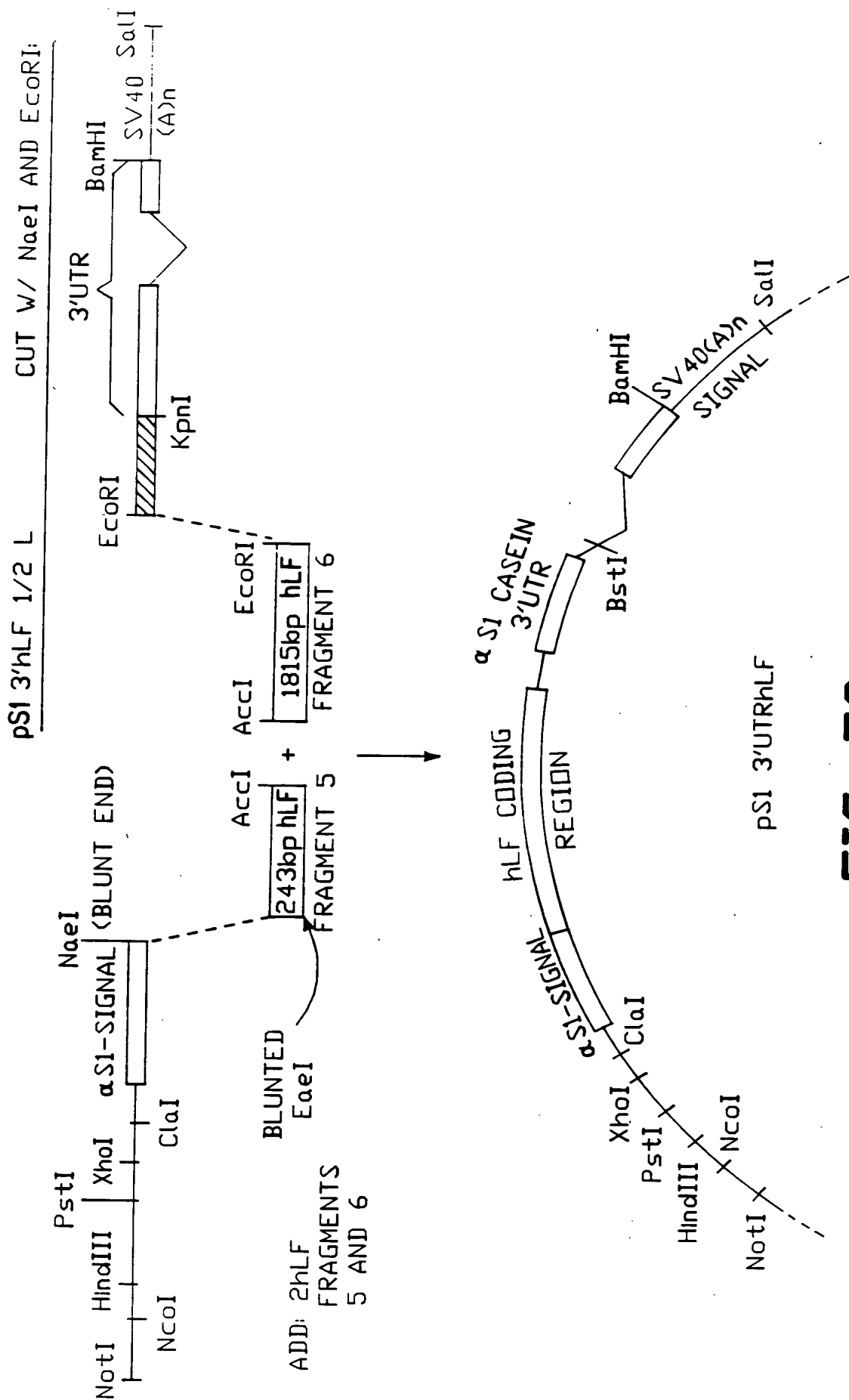


FIG.-7C

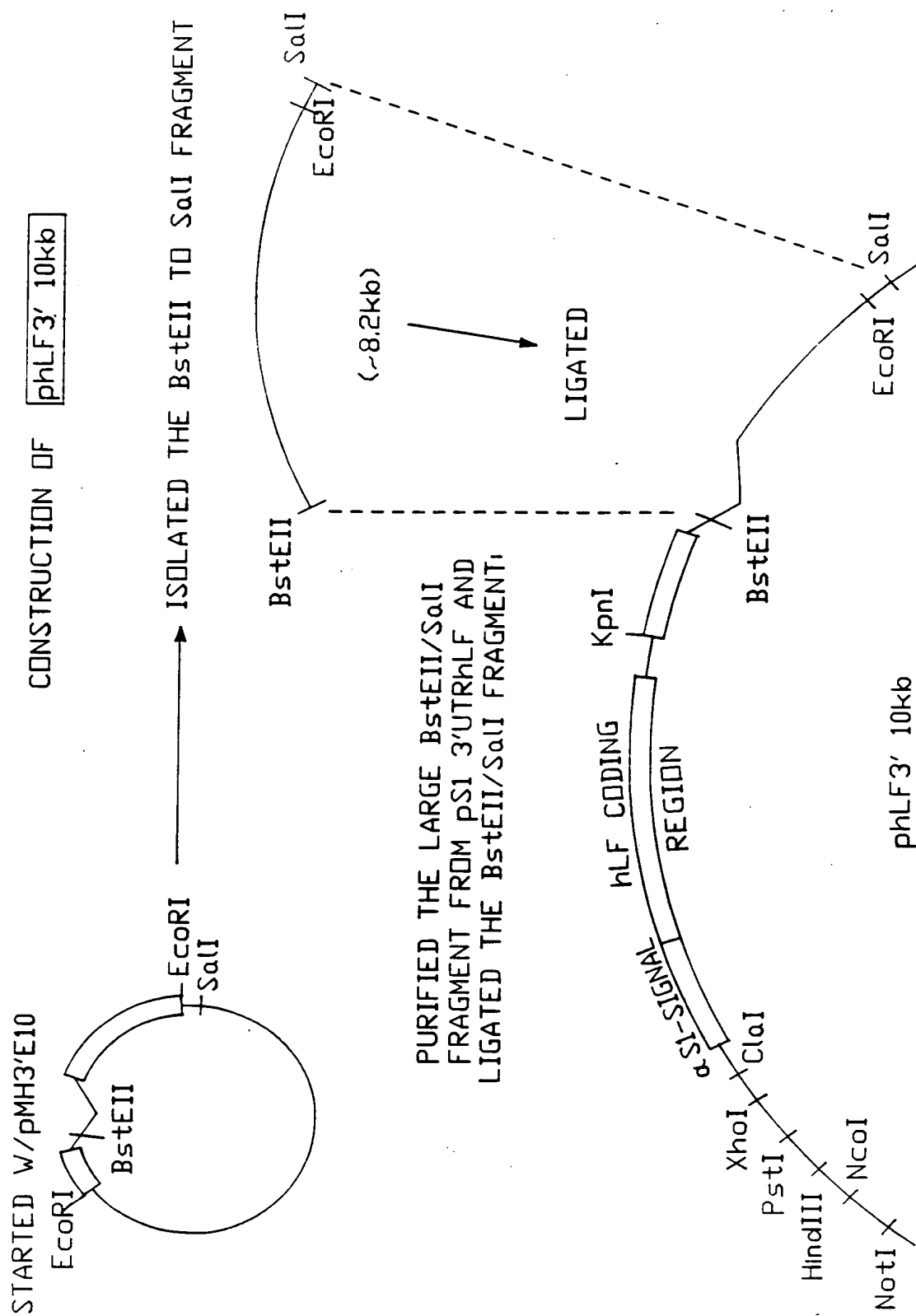
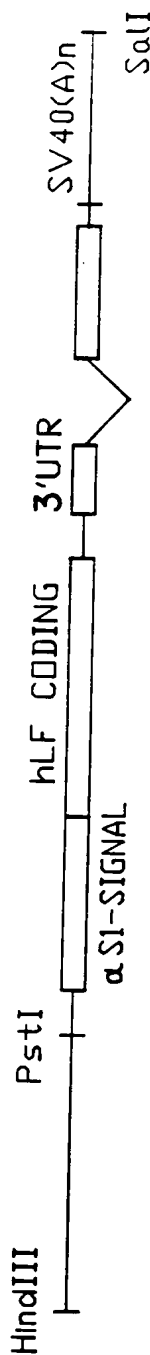


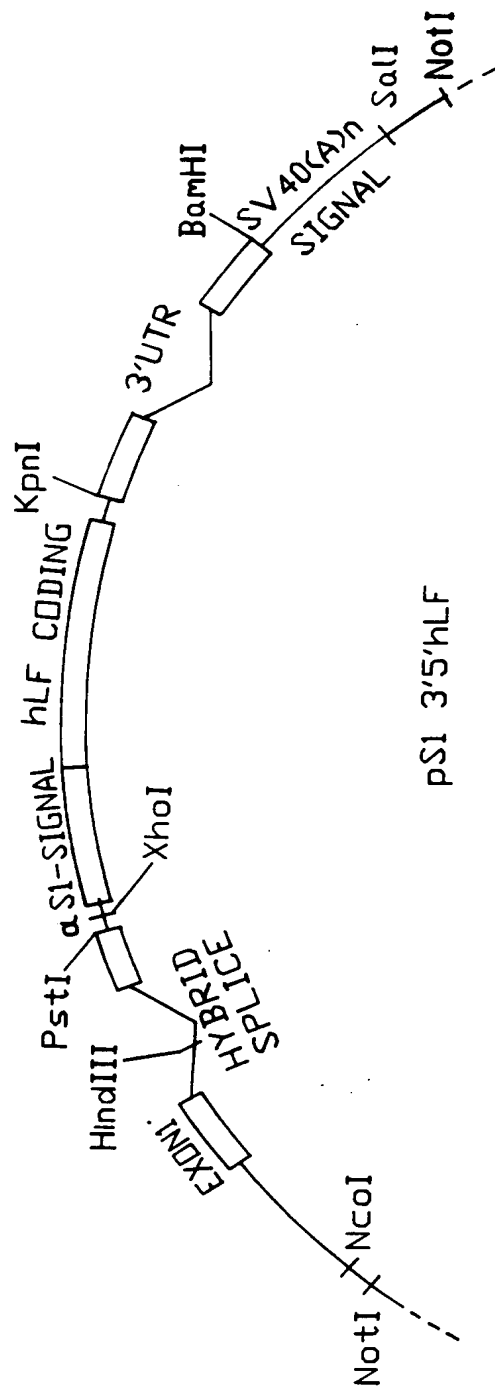
FIG.-7D

CONSTRUCTION OF **pS1 3'5'hLF**

STARTED W/pS1 3'UTRHLF. CUT W/HindIII AND SalI AND PURIFIED THIS FRAGMENT CONTAINING THE α S1-CASEIN SIGNAL SEQUENCE, hLF CODING REGION, α S1UTR AND SV40(A)_n.



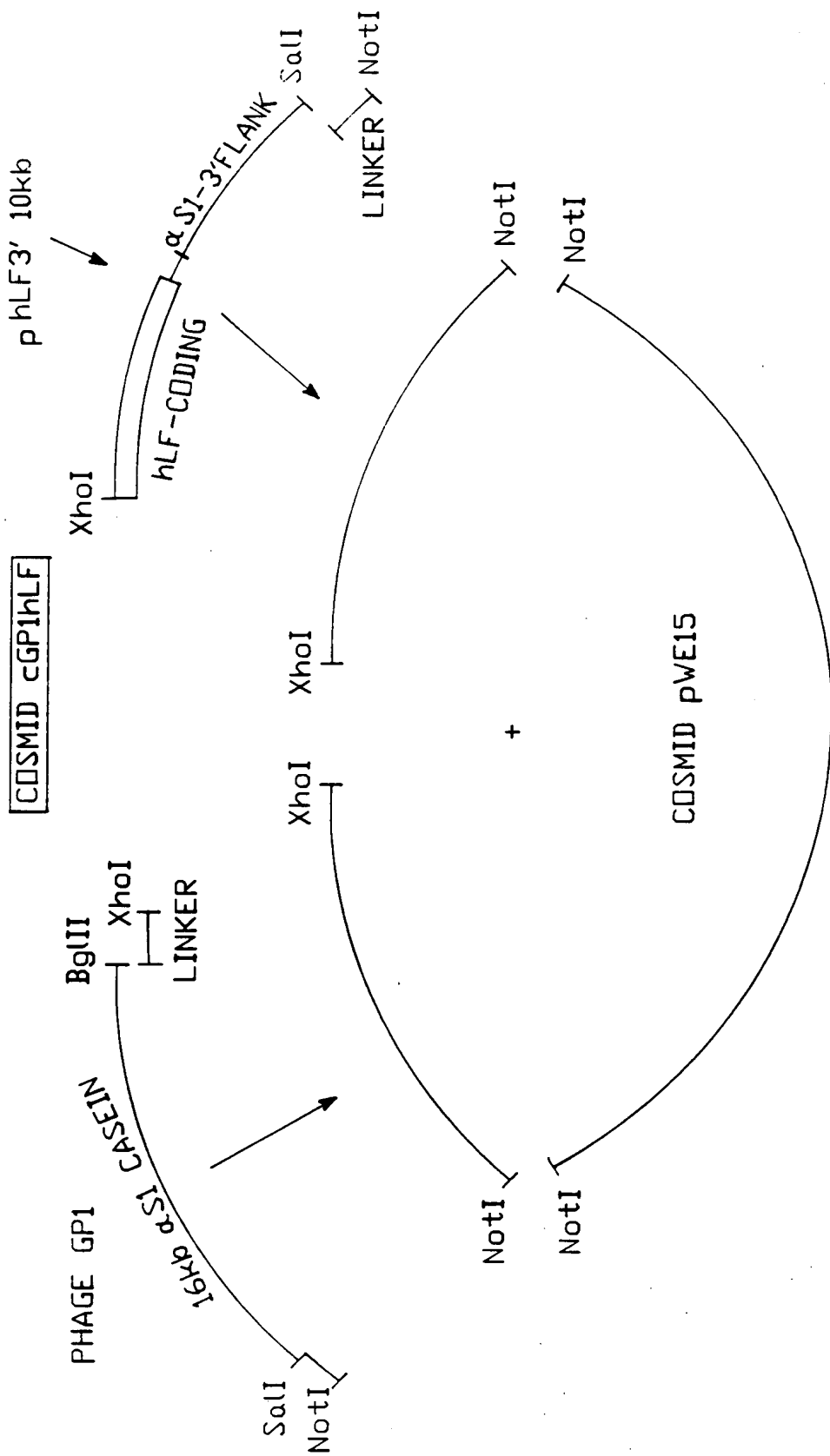
SUBCLONED INTO HindIII/SalI
CUT pMHS1 5' FLANK TO YIELD:



pS1 3'5'hLF

NOTE: **pS1 5'hLF** WAS MADE BY CUTTING **pS13'5'hLF** W/KpnI AND BamHI, FOLLOWED BY BLUNTING THE ENDS AND RELIGATING. THIS ELIMINATES THE SPLICED 3'UTR REGION.

FIG.-7E



3 WAY LIGATION. THE DNA FROM THIS COSMID IS PREPARED BY CUTTING WITH NotI AND PURIFYING THE EXPRESSION SEQUENCE PRIOR TO MICROINJECTION.

FIG.-7F

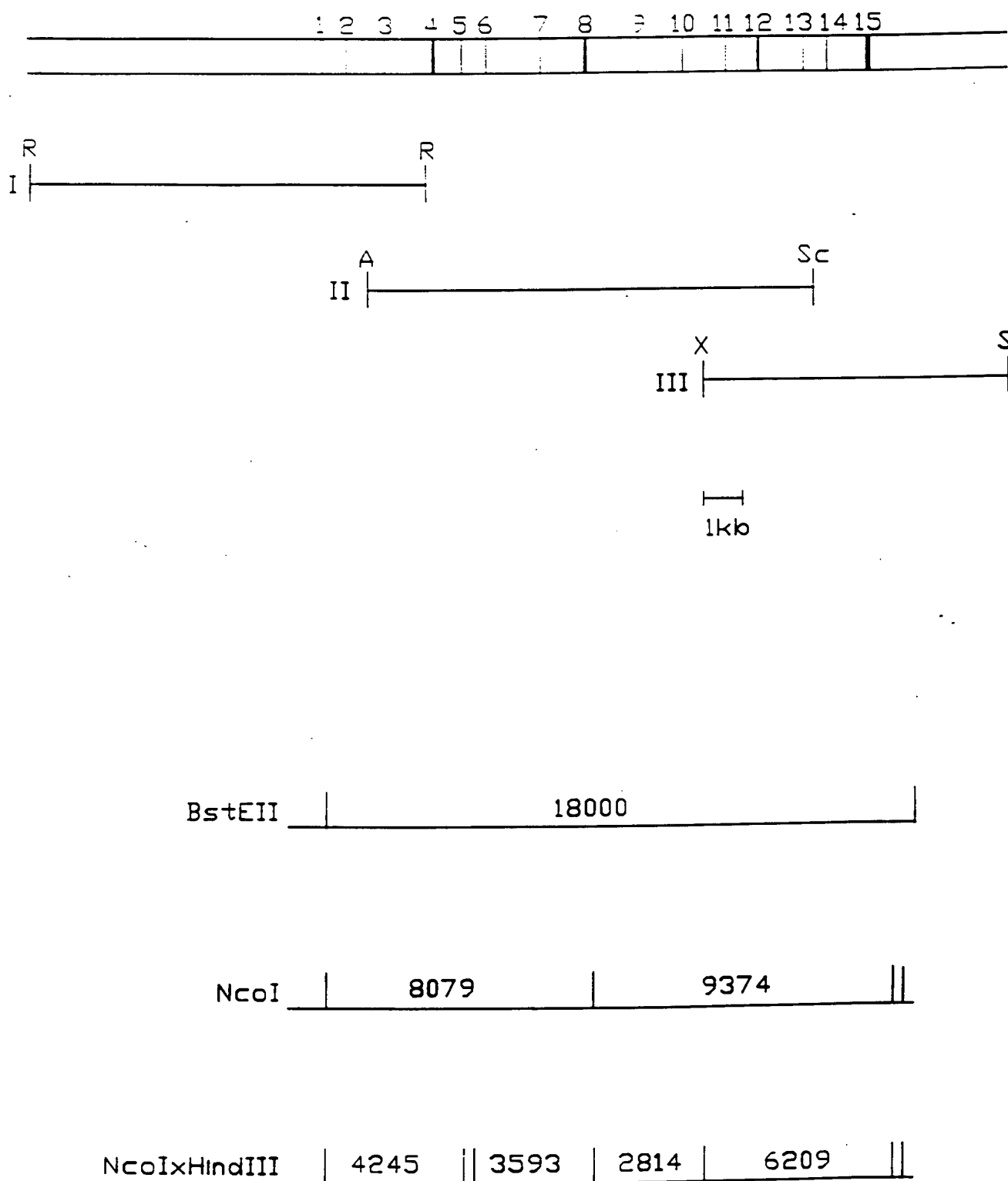
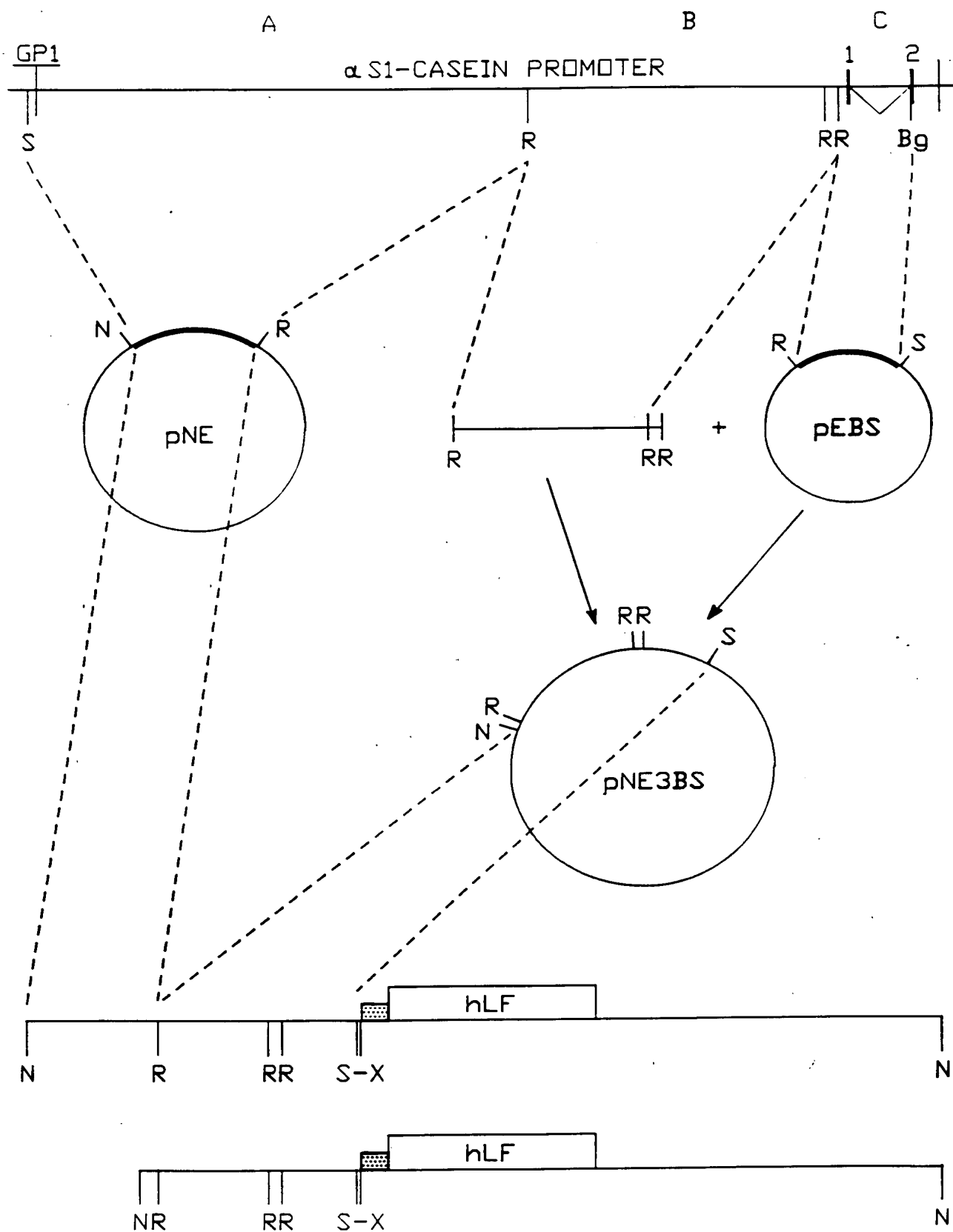


FIG.-8



S=SalI R=EcoRI Bg=BglII N=NotI X=XhoI

FIG.-9

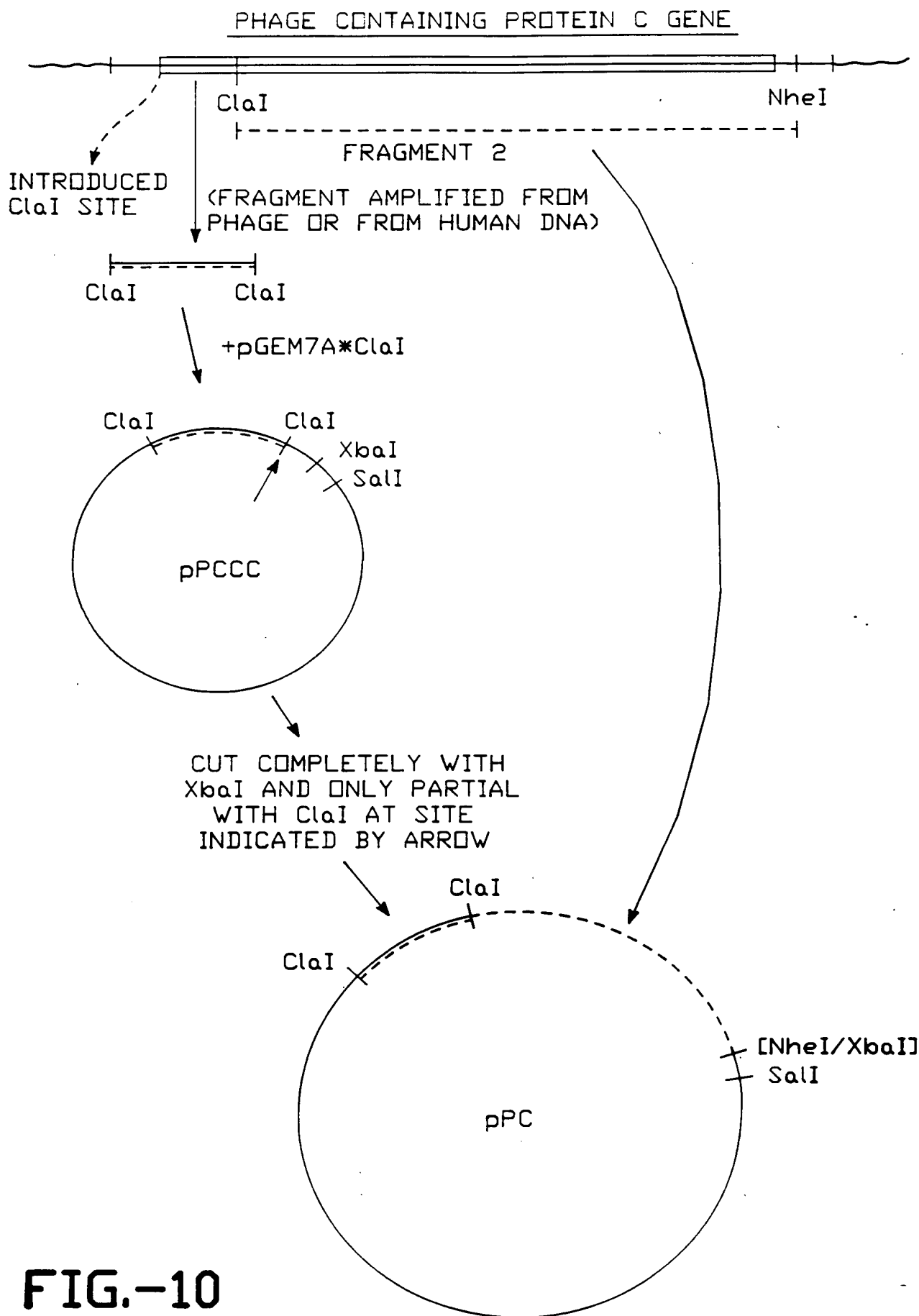


FIG.-10

5'- ATCACCTTGA TCATCAACCC AGCTTGCTGC TTCTTCCCAG
TCTTGGGTTC AAG gtattatgta tacatataac aaaatttcta tgattttcct ctgtctcacc ..
tttcattctt cactaatacg cagttgtaac ttttctatgt gattgcaagt attggtactt tcctatgata
tactgttagc aagcttgagg tgtggcaggc ttgagatctg gccatacact tgagtgacaa tgacatccac
tttgctttc tctccacag GTGTCCACTC CCAGGTCCAA CTGCAG -3'

FIG.-11

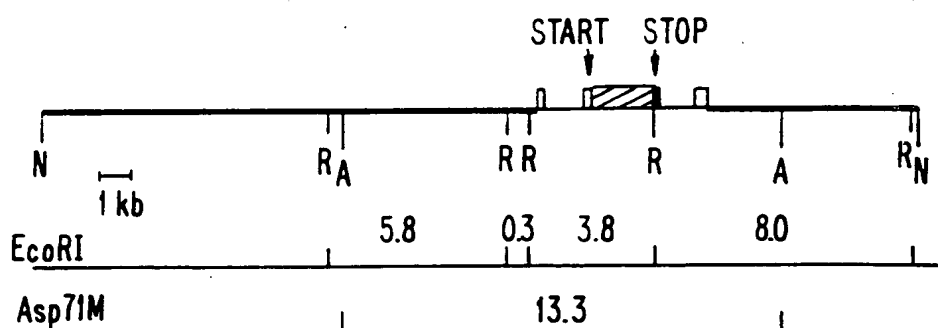


FIG. 12A.

COSMIDS CONTAINING ENTIRE hLF GENE (NOT DRAWN TO SCALE)

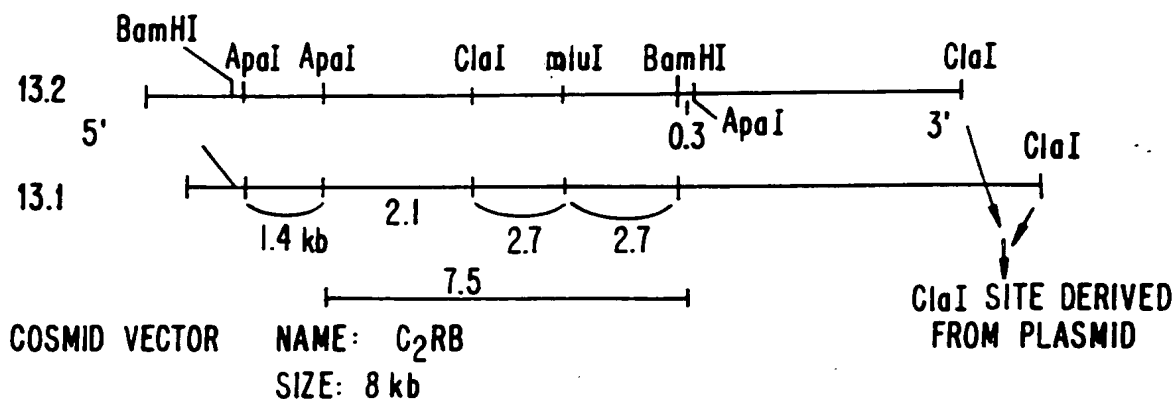


FIG. 13.

9 kb Bam HI hLF FRAGMENT IN pUC19

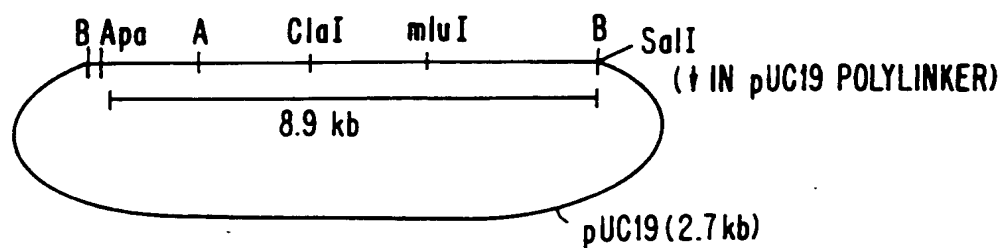
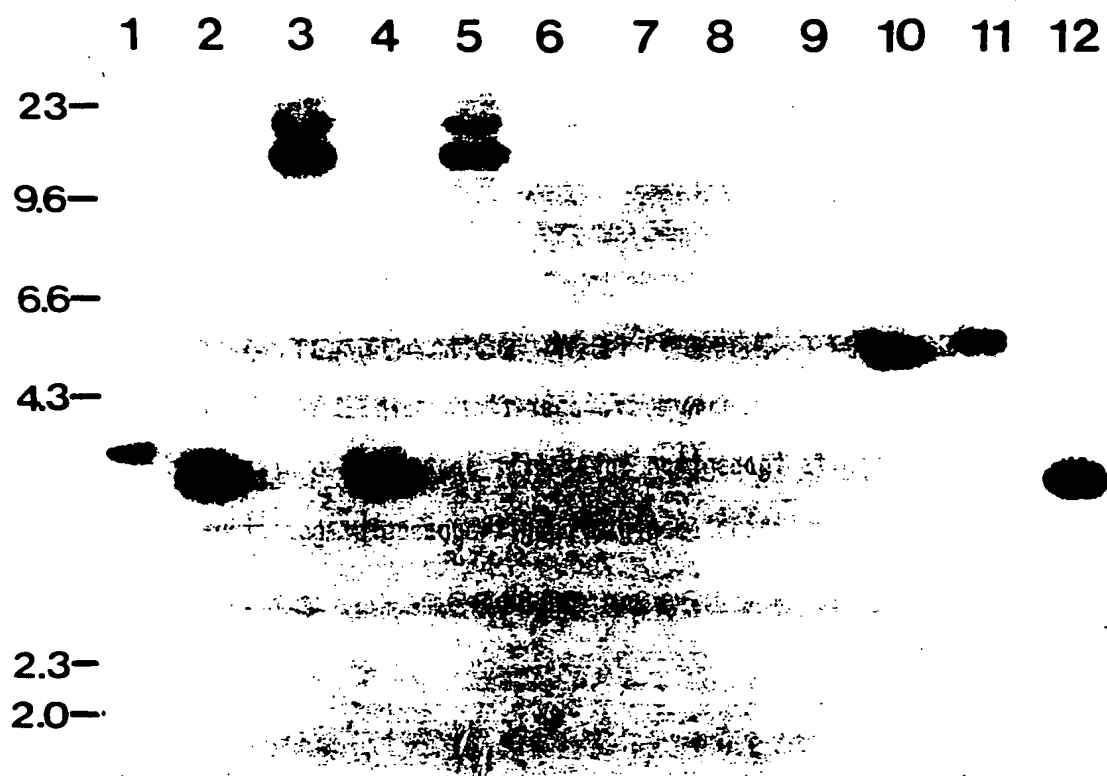
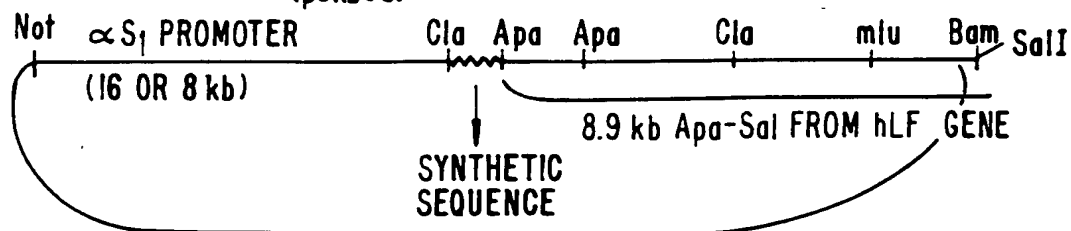


FIG. 14.

*FIG. 12B.*

LIGATION PRODUCT OF p16kbCS AND SYNTHETIC SEQ. (Cla-Apa)+ hLF FRAGMENT
(p8kbCS)



CLONING VECTOR: pkUN (4 kb)

CONSTRUCT NAME: 8 hLF gen 9k, OR 16 hLF gen.9k

FIG. 15A.

STRUCTURE OF ClaI-ApaI SYNTHETIC SEQUENCE

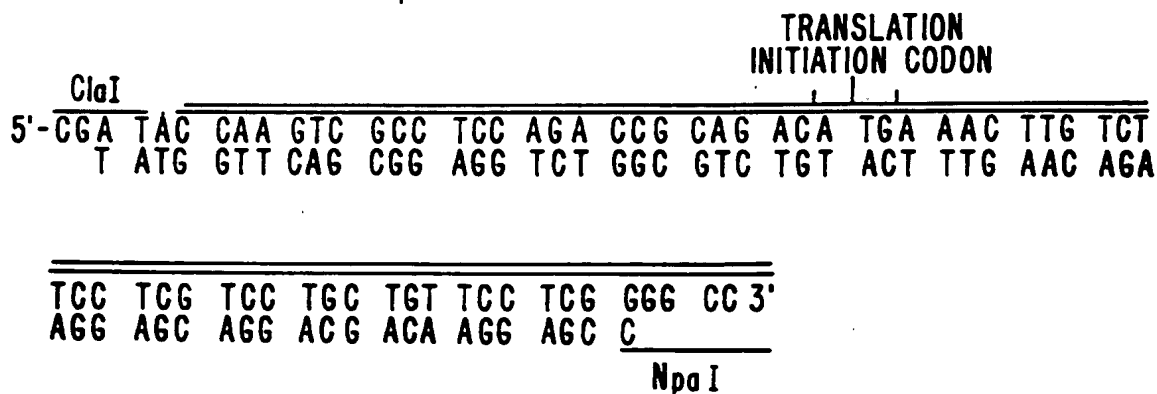
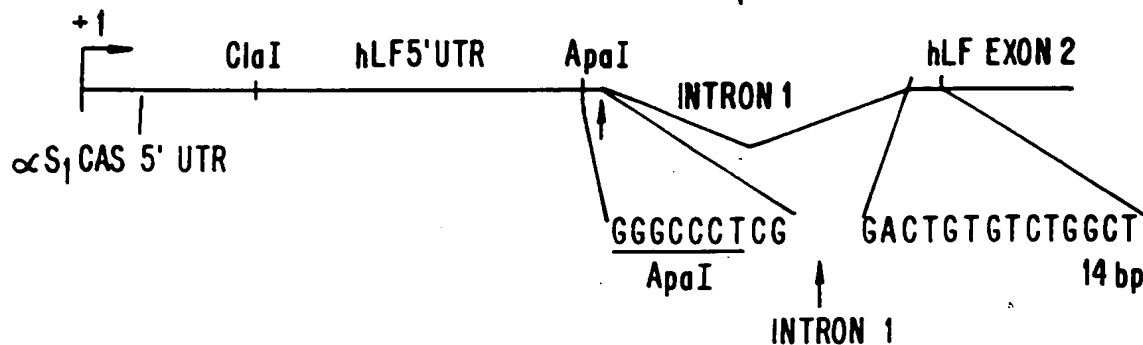


FIG. 15B.

+1: TRANSCRIPTION INITIATION SITE OF BOVINE α S₁-CASEIN GENE



STRUCTURE OF REGION CONTAINING EXON 1 (HYBRID α S₁-CASEIN/hLF EXON) AND PART OF EXON 2 OF THE GENOMIC hLF CONSTRUCTS DEPICTED IN FIGS. 15A THROUGH 17.

FIG. 15C.

COINJECTION

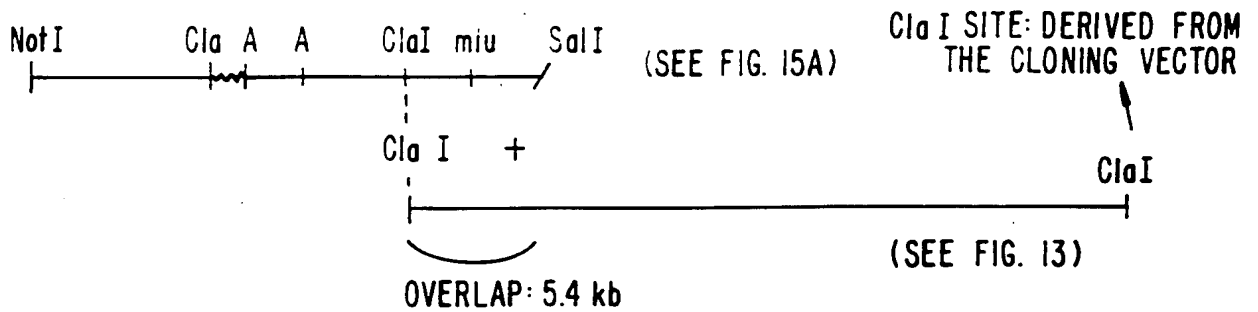
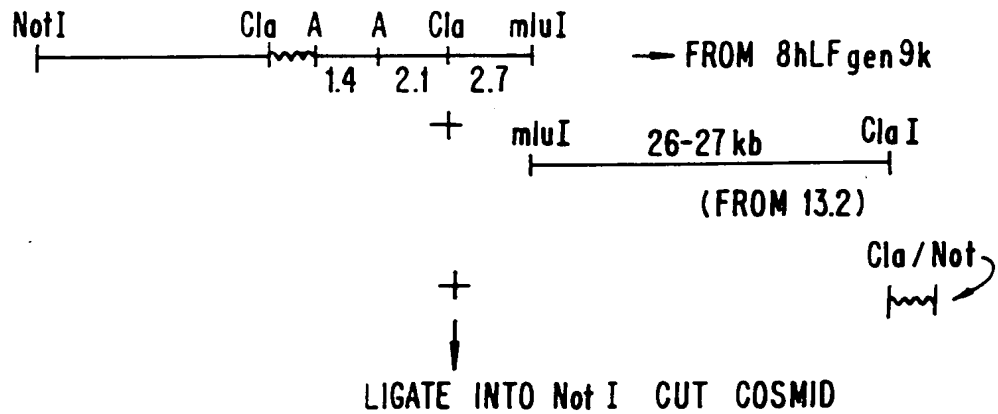


FIG. 16.

GENERATION OF 8hLF GENE



ClaI/NotI LINKER:

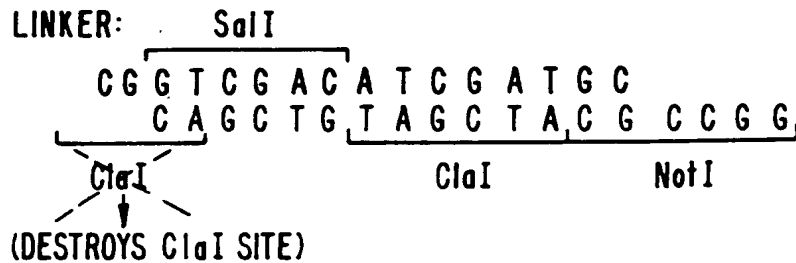


FIG. 17.

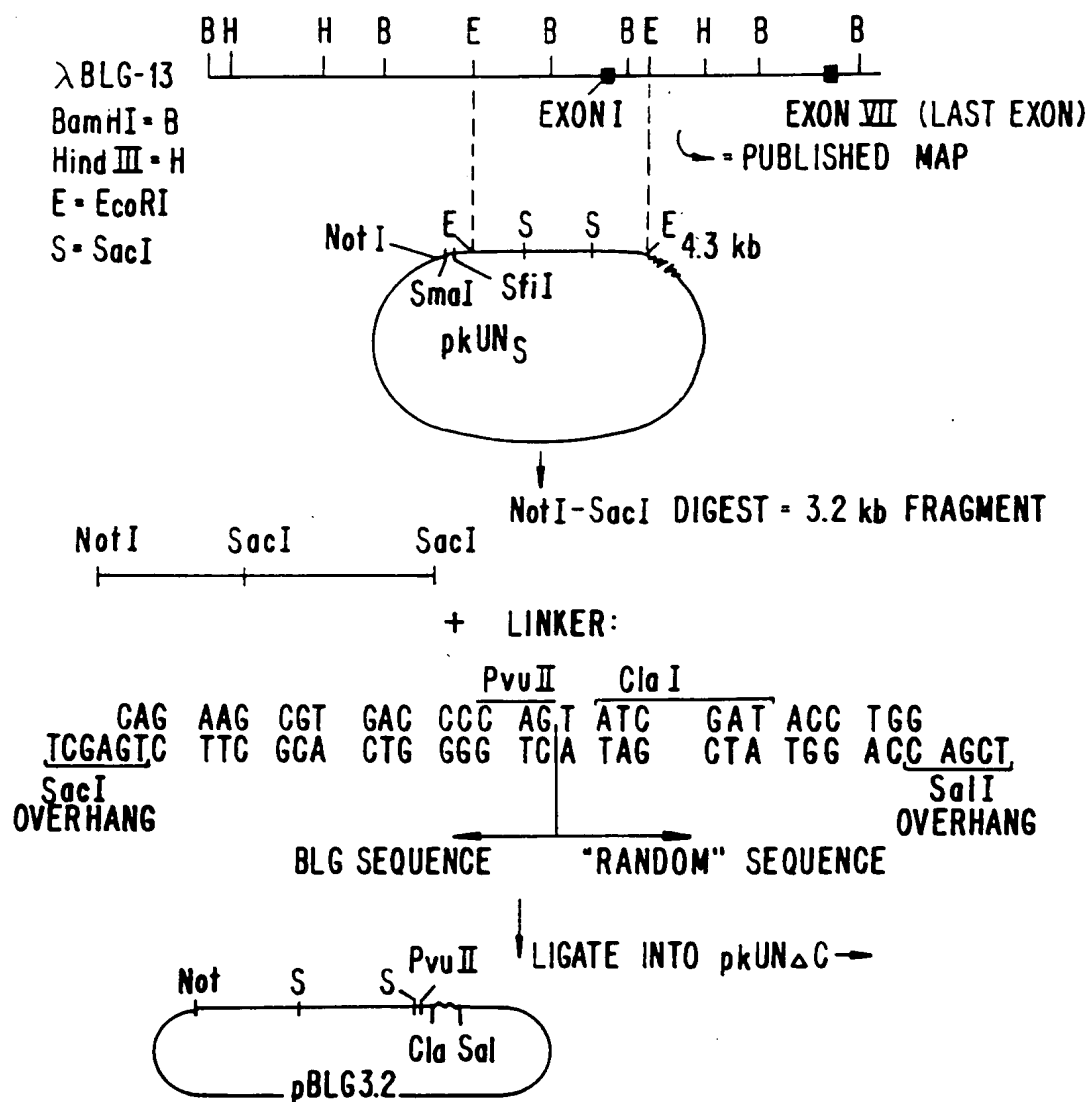


FIG. 18.

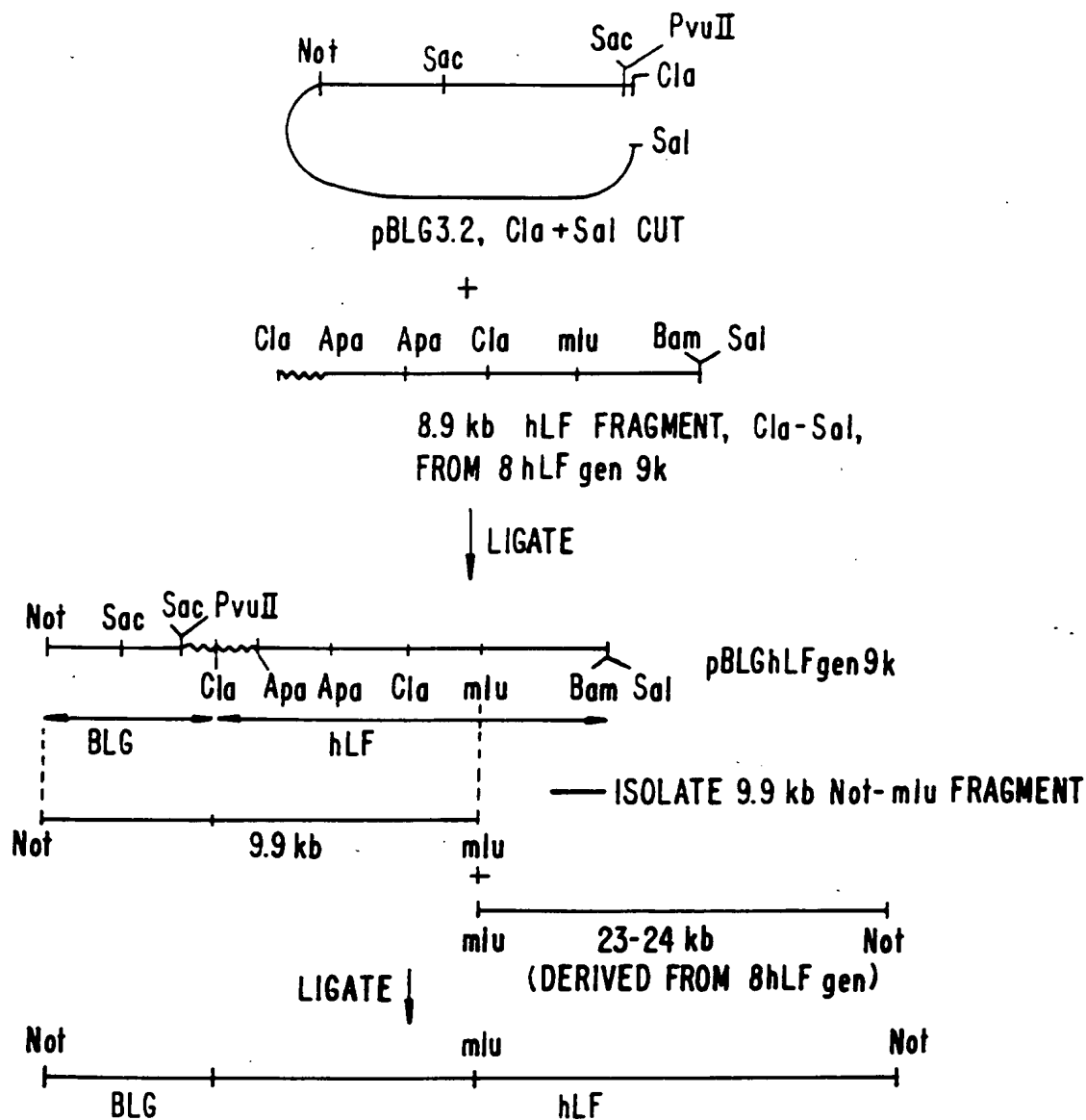


FIG. 19.

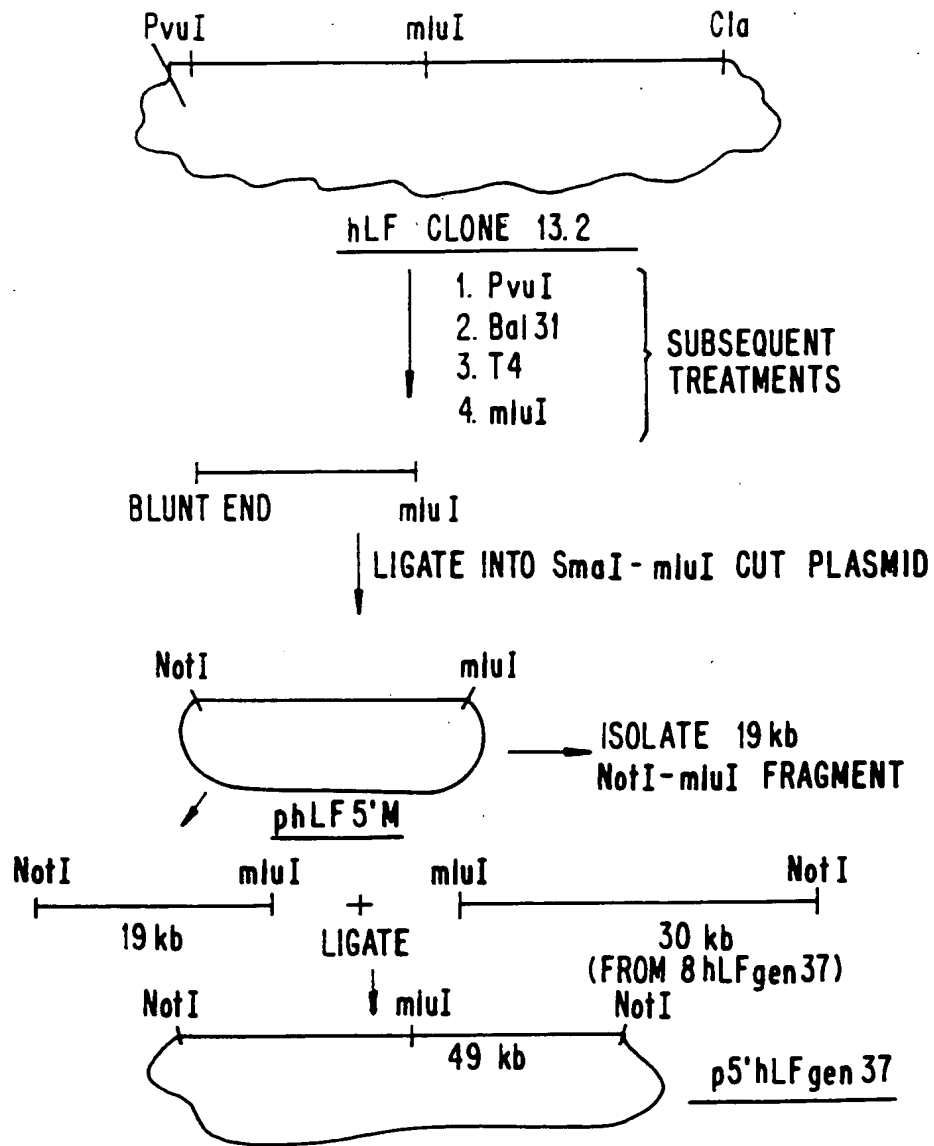


FIG. 20.

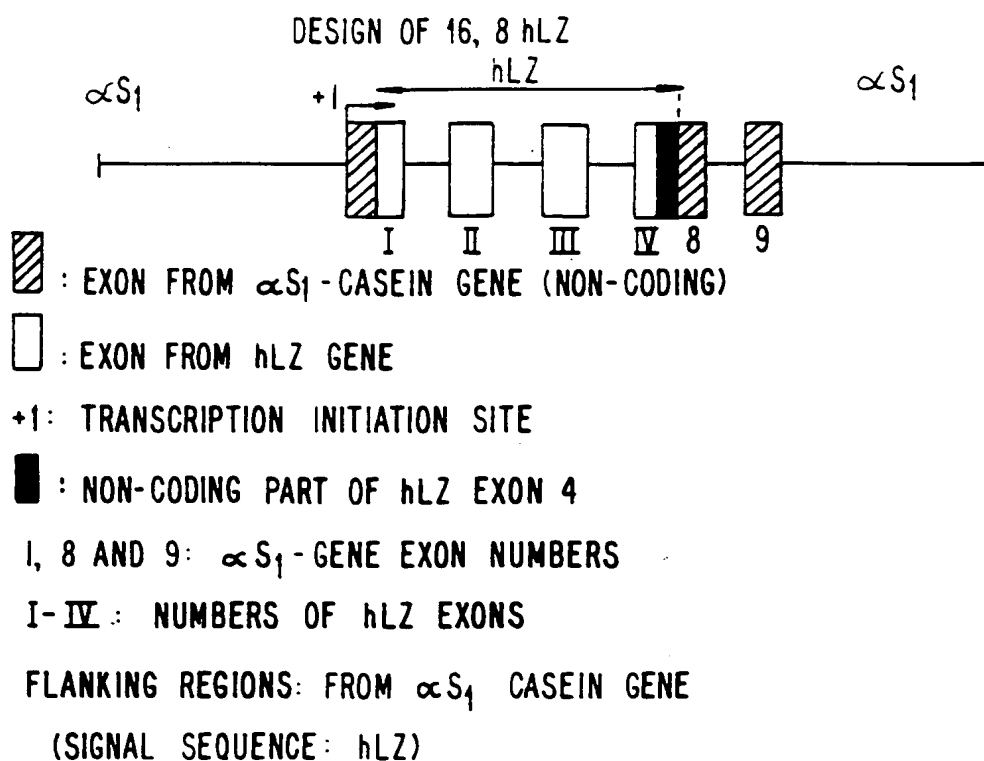


FIG. 21.

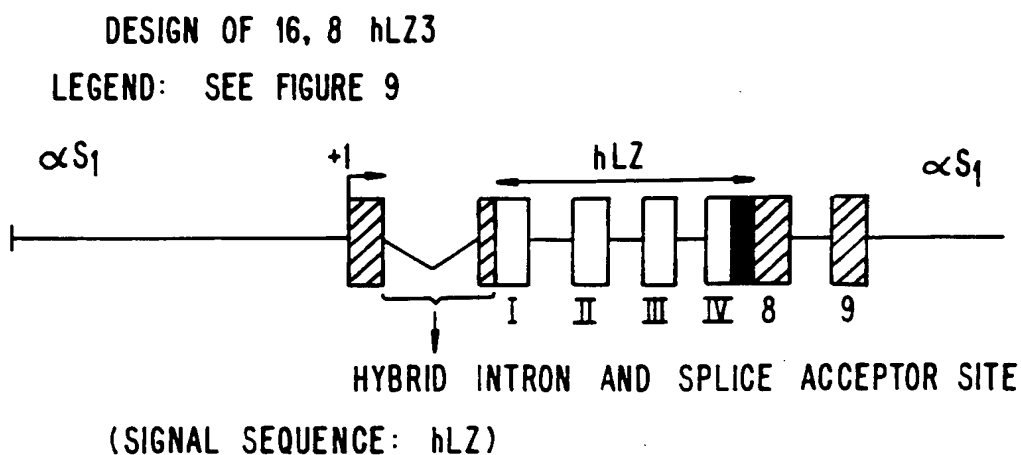
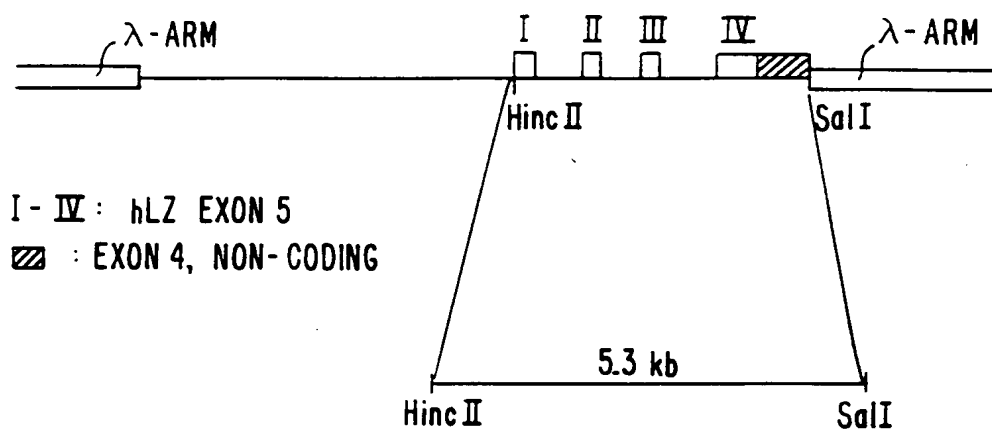
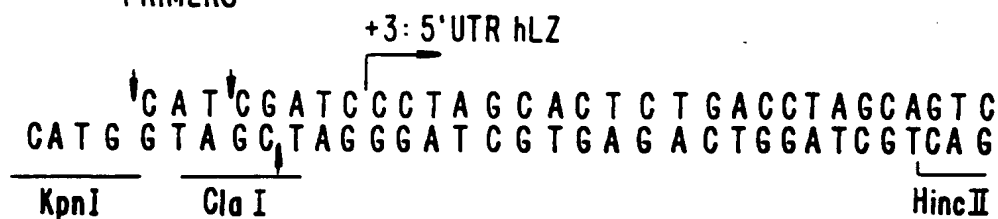


FIG. 22.

λ 7.2.1



PRIMERS:



LIGATE 5.3 Hinc II-Sal I
 Kpn-Hinc II

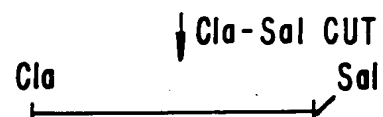
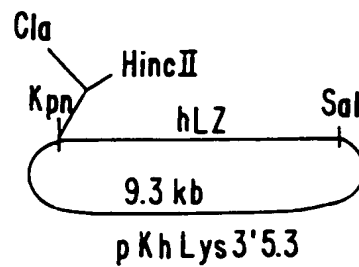


FIG. 23A.

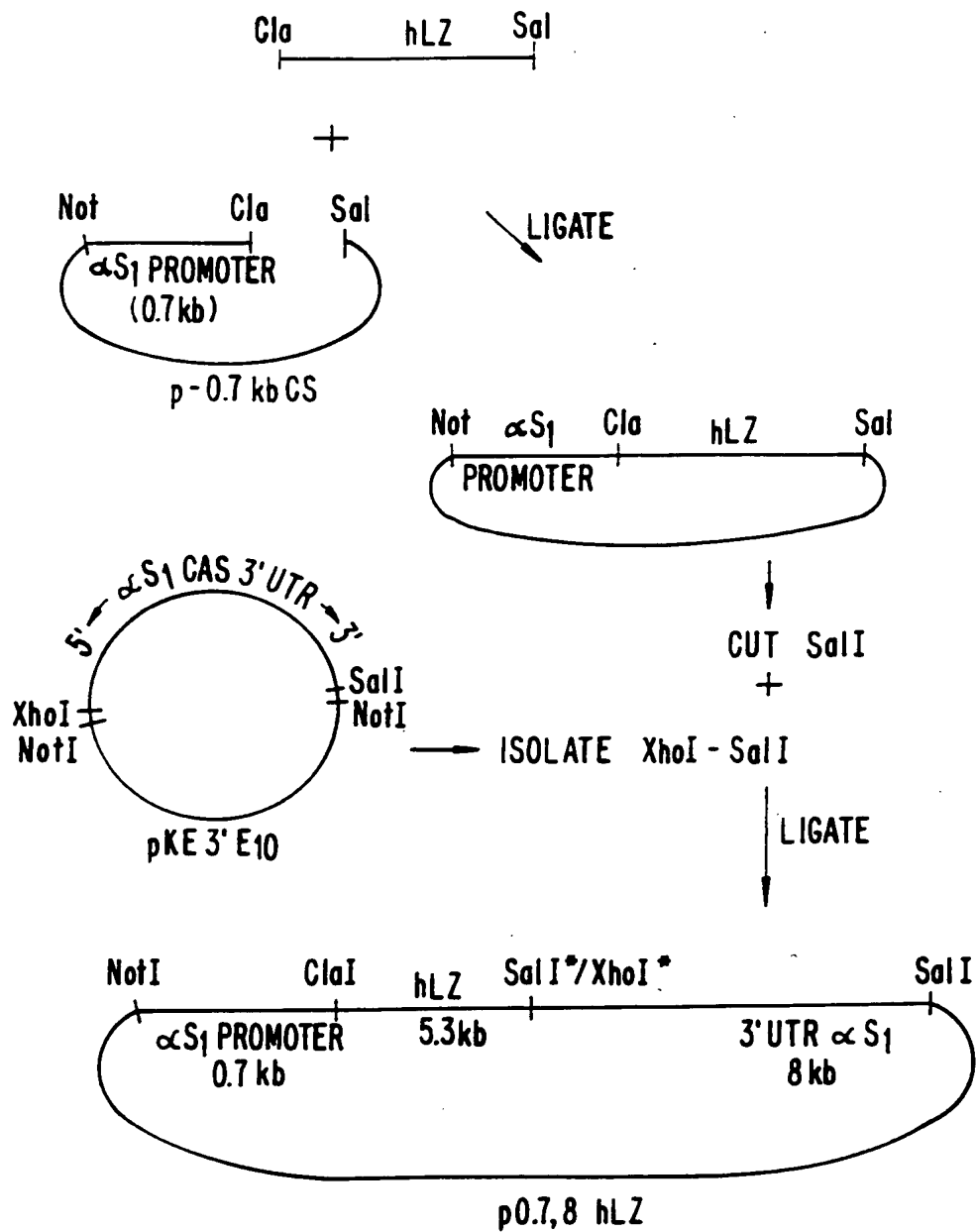


FIG. 23B.

LINKER S₁/S₂:SalI[⊗] - NotI - SalI[⊗]

⊗: = DESTROYED SITE

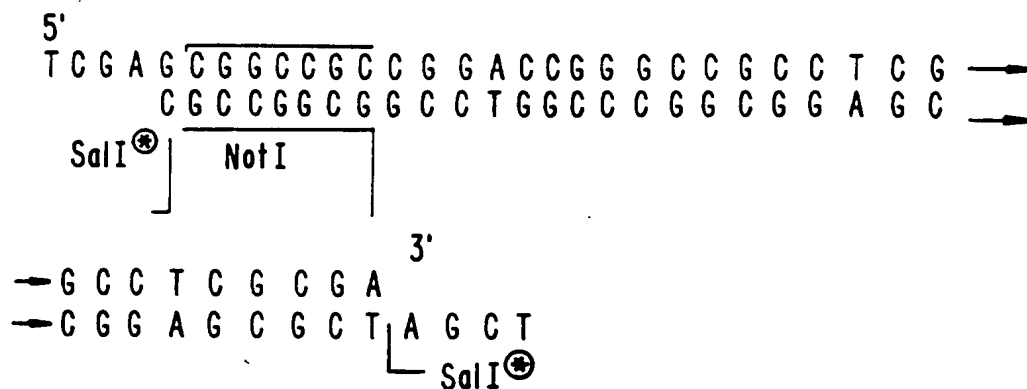


FIG. 23C.

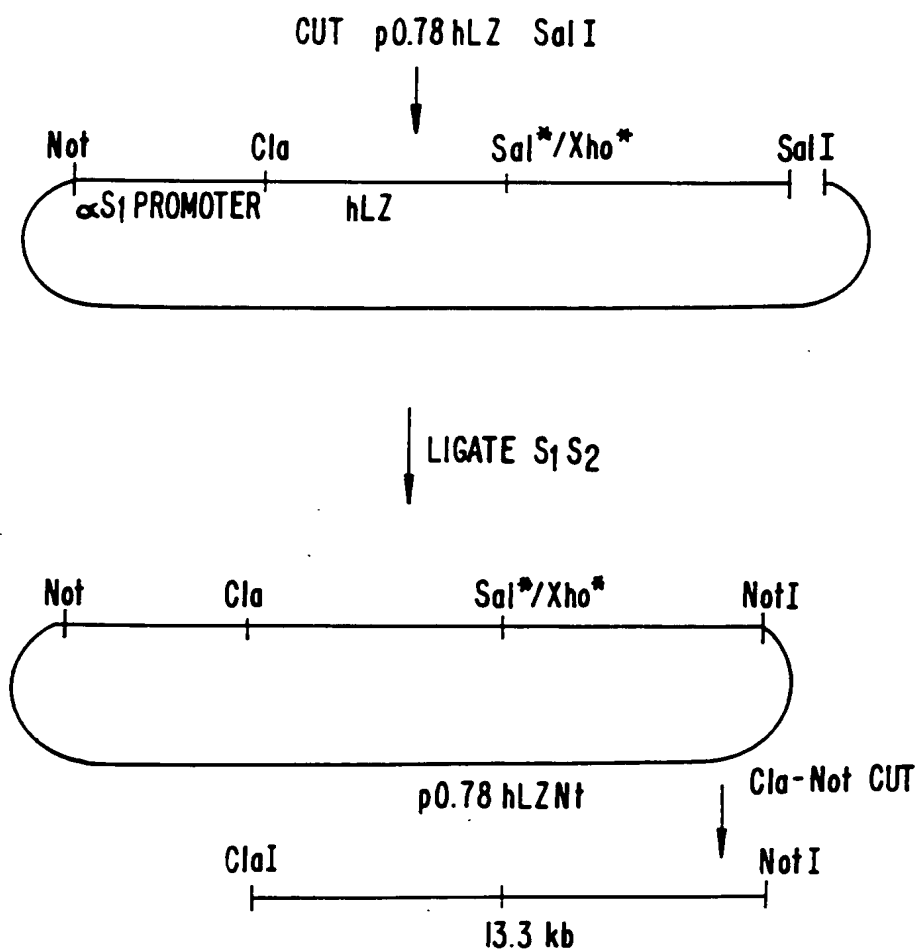
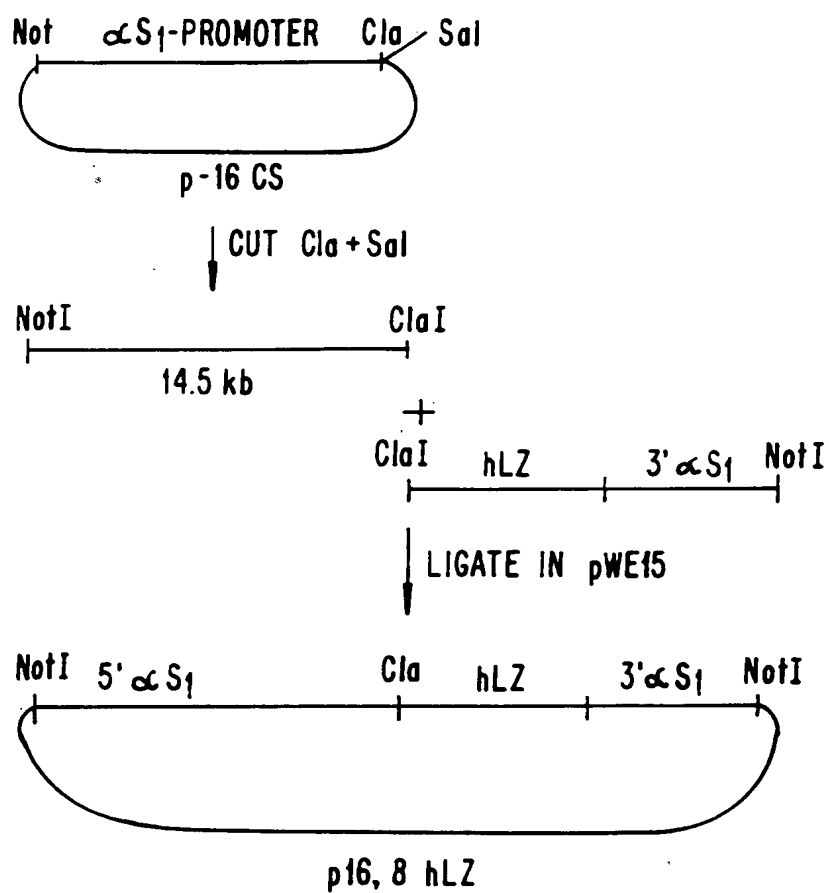


FIG. 23D.

**FIG. 23E.**

BOVINE 2 GGAAGTGCCTGGAGA...TTAAAATGTGAGAGTGGAGT...GGAGGTTG 44
 SHEEP 84 GGAAGTGTCTGCTGGGAGATTATAAATGTGAGAGGCGGGAGGTGGGAGGTTG 133
 45 GGTCTGTAGGCCTTCCCATCCCACGTGCCTCACGGAGCCCTAGTGCTAC 94
 134 GGGCCTGTGGGCCTGCCCATCCCACGTGCCTGCATTAGCCCCAGTGCTGC 183
 95 TCAGTCATGCCCCCGCAGCAGGGGTGAGGTCACTTTCCCATCCTGGGGGT 144
 184 TCAGCCGTGCCCCCGCCGAGGGGTGAGGTCACTTTCCCGTCTT.GGGGT 232
 145 TATTATGACTGTTGTCATTGTTGTTGCCATTTTTGCTACCCTAACTGGGC 194
 233 TATTATGACTCTTGTCAATTGCCATTGCCATTTTTGCTACCCTAACTGGGC 282
 195 AGCGGGTGCTTGCAGAGCCCTCGATACTGACCAGGTTCCCCCTCGGAAGC 244
 283 AGCAGGTGCTTGCAGAGCCCTCGATACCGACCAGG.TCCTCCCTCGGAAGC 331
 245 TCGACCTGAACCCCATGTCACCCTCGCCCCAGCCTGCAGAGGGTGGGTGA 294
 332 TCGACCTGAACCCCATGTCACCCTTGGCCCCAGCCTGCAGAGGGTGGGTGA 381
 295 CTGCAGAGATCCCTTTACCCAAGGCCACAGTCAATGGTTTGGAGGAGAT 344
 382 CTGCAGAGATCCCTTACCCAAGGCCACGGTCAATGGTTTGGAGGAGCT 431
 345 GGTGCCCAAGGCAGAGGCCACCTCCA.GACACACCTGCCCCCAGTGCTG 393
 432 GGTGCCCAAGGCAGAGGCCACCTCCAGGACACACCTGTCCCCCAGTGCTG 481
 394 GCTCTGACCTGTCCTTGTCTAAGAGGCTGACCCAGAAAGTGTTCCTGGCG 443
 482 GCTCTGACCTGTCCTTGTCTAAGAGGCTGACCCCGGAAGTGTTCCTGGCA 531
 444 CTGGCAGCCAGCCTGGACCCAGAGCCTGGACACCC.CCTGCGCCCCCACT 492
 532 CTGGCAGCCAGCCTGGACCCAGAGTCCAGACACCCACCTGTGCCCCCGCT 581
 493 TCTGGGGGCGTACCAGGAACCGTCCAGGCCAGAA..GGGCCTTCCTGCTT 540
 582 TCTGGGGTC.TACCAGGAACCGTCTAGGCCAGAGGGGGACTTCCTGCTT 630
 541 GGCCTCGAATGGAAGAAAGCCTCCTATTGTCCTTCGTAGAGGAAGCAACC 590
 631 GGCCTTGGATGGAAGAAAGCCTCCTATTGTCC.TCGTAGAGGAAGCCACC 679
 591 CGAGGGCCCAAGGATAGGCCAGGGGGGATTGCGGGAACCGCGTGCTT.CC 639
 680 CCGGGGCTGAGGATGAGCCAAGTGGGATTCCGGGAACCGCGTGCTTGGG 729
 640 GCGGCGGGCCGGGCTGGCTGGCTGGC..CCTCCTCCTGTATAAGGCCCGG 687
 730 GGGCCAGCCGGGCTGGCTGGCTGCATGCGCCTCCTGTATAAGGCCCA 779

FIG. 24

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688 AGCCCG. CTGTCTCAGCCCTCCACTCCCTGCAGAGCTCAGAAGCGTGACC 736
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
780 AGCCTGCCTGTCTCAGCCCTCCACTCCCTGCAGAGCTCAGAAGCACGACC 829
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
737 CCAGCTGCAGCCATGAAGTGCCTCCTGCTTGC.....CCTGGCCCTCAC 780
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
830 CCAGCTGCAGCCATGAAGTGCCTCCTGCTTGGCCCTGGGCCTGGCCCTCGC 879
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
781 CTGTGGCGCCCAAGGCCCTCATCGTCACC 808
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
880 CTGTGGCGTCCAGGCCATCATCGTCACC 907
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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* TRANSLATION INITIATION CODON

FIG. 24 [continued]

LINKER GP 278/279

TRANSLATION START SITE (αS_1 SIGNAL SEQUENCE)
ClaI
 CGATAACCATGAACTTCTTATCCTCACCTGTCTTGTGGCTGTTGCTCTTG
 |
 TATT — ETC.

αS_1 — HLZ SEQUENCE
 — CCAAGGTCTTTGAAAGGTGTGAGTTGC
 ETC. — AACC

FIG. 25.

CONSTRUCTION OF 16.8 A hLZ3:

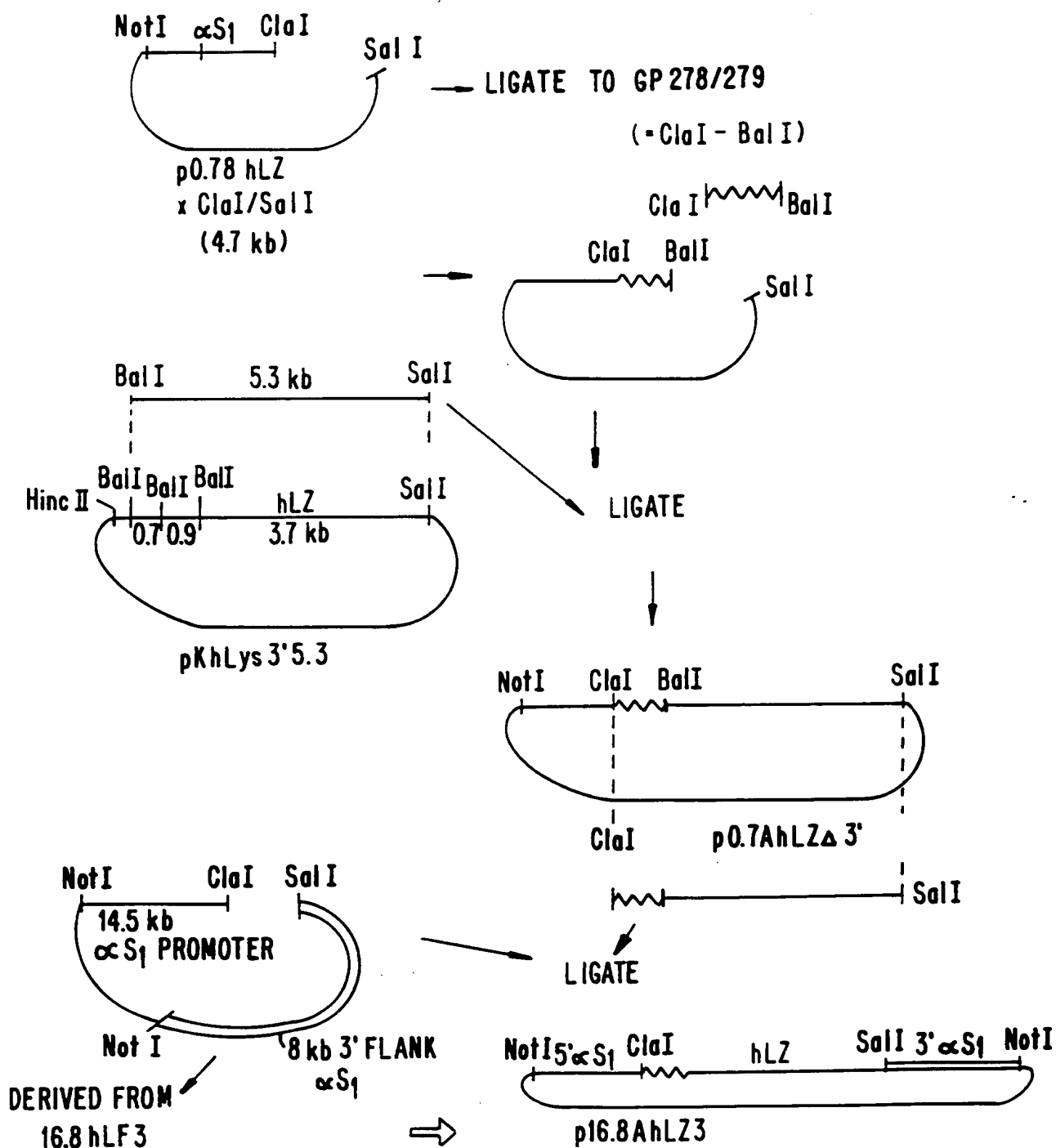


FIG. 26.

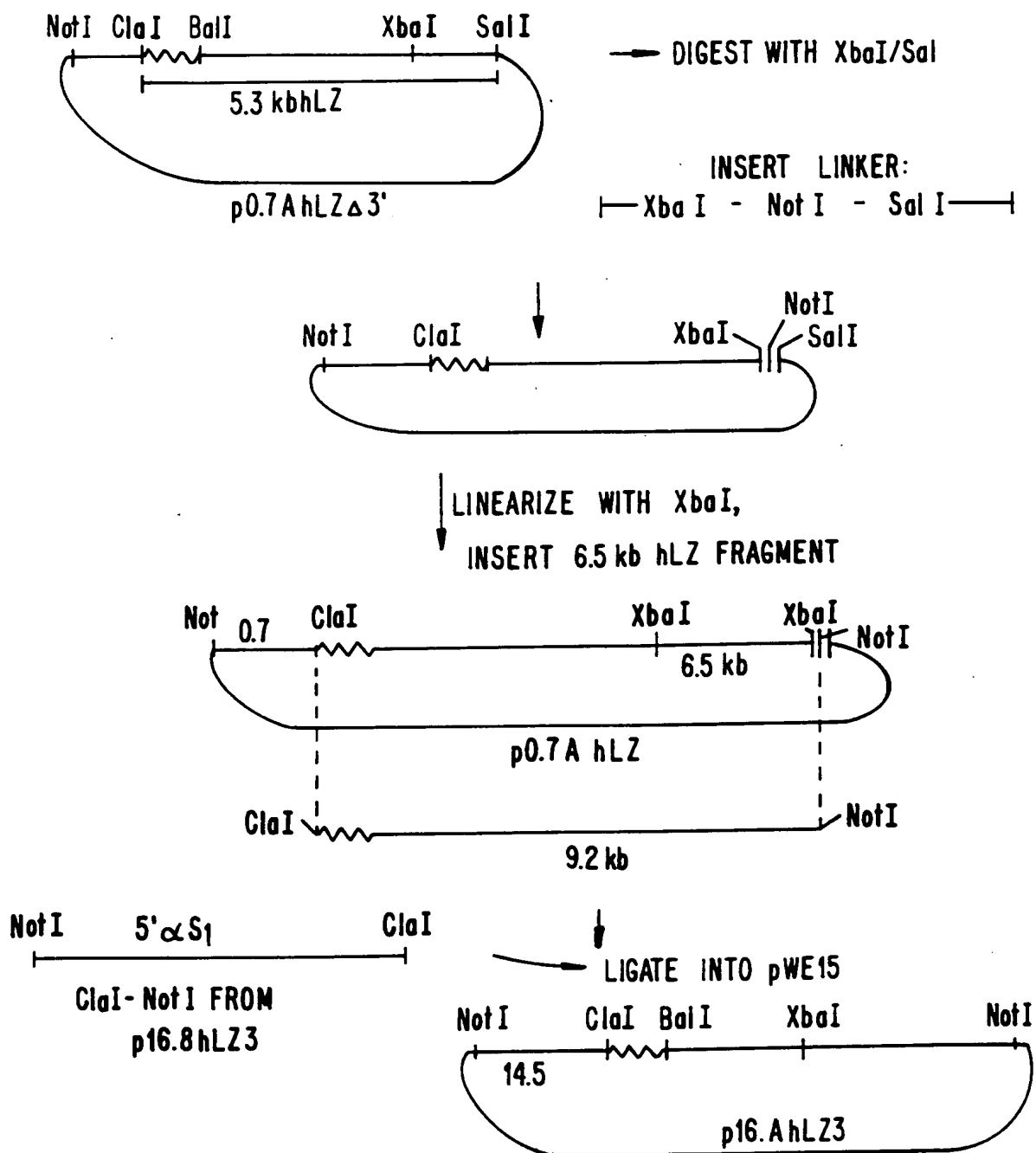
CONSTRUCTION OF 16 A hLZ3:

FIG. 27.